

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 62.1321 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773A-11

Perfect score: 688

Sequence: 1 MSPAQFLFLVLVIQETNGD.....VOGTHFPHFGGKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: geneseq1980s.*
- 2: geneseq1990s.*
- 3: geneseq2000s.*
- 4: geneseq2001s.*
- 5: geneseq2002s.*
- 6: geneseq2003as.*
- 7: geneseq2003bs.*
- 8: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	100.0	132	6	ABG74244 Mouse ant
2	644	93.6	238	8	ADP45549 Mouse bin
3	638	92.7	238	8	ADM72033 Chimeric
4	636	92.4	132	5	ABG76923 Mouse 3D6
5	636	92.4	132	8	ADR88406 Murine 3D
6	630	91.6	135	5	ABG79729 Anti-Stre
7	626	91.0	133	8	ADO0819 Antibody
8	626	91.0	133	8	ADO43845 Light cha
9	620	90.1	239	6	ABP58274 Humanised
10	617	89.7	132	2	AAR12361 Light (ka
11	616	89.5	239	7	ADD47025 Rat Prote
12	615	89.4	131	2	AAR12239 Mouse MAB
13	608	88.4	132	2	AAR24712 Sequence
14	601	87.4	132	5	ABG76931 Humanised
15	601	87.4	132	8	ADR88415 Humanised
16	599	87.1	238	8	ADM72035 Chimeric
17	596	86.6	142	4	AAE07032 Murine an
18	596	86.6	142	8	ADQ89324 Mouse imm
19	592	86.0	132	5	ABG76925 Humanised
20	592	86.0	132	8	ADR88409 Humanised
21	580	84.3	239	2	AAR24811 Sequence
22	574	83.4	112	6	ABB99636 2A2 monoc
23	565	82.1	113	3	AAU76445 Mouse mon
24	565	82.1	113	3	AAB12170 Mouse HBV
25	560	81.4	112	7	ADE13218 Humanised

26	560	81.4	113	8	ADQ76082	Adq76082 Heterorec
27	560	81.4	113	8	ADQ76086	Adq76086 Heterorec
28	559	81.2	113	8	ADQ76076	Adq76076 Heterorec
29	557	81.0	113	8	ADQ76088	Adq76088 Heterorec
30	557	81.0	113	8	ADQ76090	Adq76090 Heterorec
31	556	80.8	113	8	ADQ76078	Adq76078 Heterorec
32	555	80.7	132	2	AAW79225	AAW79225 Humanised
33	555	80.7	132	2	AAW56349	AAW56349 Humanised
34	555	80.7	132	2	AAAY30186	AAAY30186 Sequence
35	555	80.7	257	3	AAB09777	AAB09777 Antiviral
36	554	80.5	113	8	ADQ76092	Adq76092 Heterorec
37	554	80.5	113	8	ADQ76080	Adq76080 Heterorec
38	553	80.4	113	3	AAB12171	AAB12171 Humanised
39	553	80.4	113	4	AAE03751	AAE03751 Murine PS
40	553	80.4	218	4	AAE03756	AAE03756 Chimeric
41	552	80.2	122	8	ADJ95990	ADJ95990 Immunoglo
42	552	80.2	130	8	ADJ95992	ADJ95992 Immunoglo
43	551	80.1	112	8	ADQ76094	Adq76094 Heterorec
44	550	79.9	113	8	ADQ76084	Adq76084 Heterorec
45	548	79.7	113	8	ADG25828	ADG25828 Anti-CD30

ALIGNMENTS

RESULT 1

ABG74244

ID ABG74244 standard; protein; 132 AA.

AC ABG74244;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3D8 light chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;

XX immunostimulant; GB3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

XX 3E11; prostate-specific membrane antigen; zeta signalling chain;

XX CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

XX small cell lung cancer; light chain variable region; mouse.

OS Mus sp.

XX US2002132983-A1.

PN 19-SEP-2002.

PD 10-DEC-2001; 2001US-00006773.

PP 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

PA (JUNG/) JUNGHANS R P.

XX Junghans RP;

PI WPI; 2003-2089946/20.

DR N-PSDB; ABX16570.

XX New chimeric molecule useful in treating patients with disorders, such as

XX melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 13; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GP3

XX (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

XX variable gene sequences, or the PSMA (prostate-specific membrane antigen)

XX binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

XX sequences, the zeta signalling chain of the T cell receptor and an

XX intervening CD8alpha hinge in which cysteine residues have been mutated.

XX The chimaeric molecules expressed in T cells or NK cells or other

XX effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3D8 light chain variable region
 XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 688; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 3.8e-55;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIWQETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
 DB 1 MSPAQFLFLVLIWQETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
 QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFP 120
 DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFP 120
 QY 121 TFGGGTKLEIKR 132
 DB 121 TFGGGTKLEIKR 132

RESULT 2
 ADP45549
 ID ADP45549 standard; protein; 238 AA.
 XX
 AC ADP45549;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.
 XX
 KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
 KW nerve repair; neuroprotective; gene therapy;
 KW central nervous system injury; CNS injury; neurodegenerative disorder;
 KW mouse; antibody.
 XX
 OS Mus musculus.
 XX WO2004052932-A2.
 PN
 XX
 PD 24-JUN-2004.
 XX
 PF 09-DEC-2003; 2003WO-EP013960.
 XX
 PR 10-DEC-2002; 2002GB-00028832.
 XX

(NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
 PI Zurini M;
 XX
 DR WPI; 2004-468818/44.
 XX
 PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
 PT D20 or NogoA623-640, useful in preparing a composition for treating CNS
 PT injury or neurodegenerative disorders.
 XX

PS Claim 9; SEQ ID NO 3; 121pp; English.
 XX
 CC The present invention describes a binding molecule which binds to human
 CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a
 CC dissociation constant of less than 100nM. Also described: (1) a
 CC polynucleotide encoding the binding molecule; (2) an expression vector or
 CC system comprising the polynucleotide; (3) a host cell comprising the
 CC expression system; (4) a pharmaceutical composition comprising the

CC binding molecule and a carrier or diluent; and (5) treating diseases
 CC associated with nerve repair. The binding molecule has neuroprotective
 CC activity, and can be used in gene therapy. The binding molecule is useful
 CC in preparing a composition for treating central nervous system (CNS)
 CC injury or neurodegenerative disorders. The present sequence represents a
 CC mouse binding molecule 11C7 light chain, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 238 AA;

Query Match 93.6%; Score 644; DB 8; Length 238;
 Best Local Similarity 92.4%; Pred. No. 7.8e-51;
 Matches 122; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIWQETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
 DB 1 MSPAQFLFLVLIWQETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
 QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFP 120
 DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFP 120
 QY 121 TFGGGTKLEIKR 132
 DB 121 TFGGGTKLEIKR 132

RESULT 3
 ADM72033
 ID ADM72033 standard; protein; 238 AA.
 XX
 AC ADM72033;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Chimeric mouse-human antibody M3C11 light chain.
 XX
 KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
 KW cytotostatic; M3C11.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX WO2004022739-A1.
 PN
 XX
 PD 18-MAR-2004.
 XX
 PF 04-SEP-2003; 2003WO-JP011318.
 XX
 PR 04-SEP-2002; 2002WO-JP008999.
 XX

(CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
 XX
 DR WPI; 2004-269573/25.
 DR N-PSDB; ADM72032.
 XX
 PT Antibody against the N terminus of glypican 3(GPC3) causes cell
 PT disruption and is useful as an anticancer agent.
 XX
 PS Example 4; SEQ ID NO 18; 122pp; Japanese.
 XX

CC The invention relates to an antibody against the N terminus of glypican 3
 CC (GPC3). The antibody can be used for causing cell disruption and can be
 CC used as an anti-cancer agent. The present sequence represents a chimeric
 CC mouse-human antibody M3C11 light chain.
 XX
 SQ Sequence 238 AA;

Query Match 92.7%; Score 638; DB 8; Length 238;
 Best Local Similarity 93.2%; Pred. No. 2.8e-50;

CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 3D6
CC immunoglobulin light chain variable region.
XX
XX Sequence 132 AA;

Query Match 92.4%; Score 636; DB 8; Length 132;
Best Local Similarity 93.9%; Pred. No. 2.2e-50;
Matches 133; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGDVVMTQPLTSLVTIGQPASISCKSSQSLDSGKTYLNL 61
QY 61 LORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRVEADLGVYVCVQGTTHPPH 120
DB 62 LORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRVEADLGLYVCVQGTTHPPR 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 6
ABB79729
ID ABB79729 standard; protein; 135 AA.
XX
AC ABB79729;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAB SWLA3 VL.
XX
KW Streptococcus mutans; monoclonal antibody; MAB; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.
XX
OS Mus musculus.
XX US2002068066-A1.
XX
PN 06-JUN-2002.
XX
PD 15-JUN-2001; 2001US-00881823.
XX
PF 20-AUG-1999; 99US-00378577.
XX
PR (SHIW/) SHI W.
XX (MORR/) MORRISON S L.
XX (TRIN/) TRINH K.
XX (WIMS/) WIMS L.
XX (CHEN/) CHEN L.
XX (ANDE/) ANDERSON M H.
XX
XX Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX WPI: 2002-565838/60.
XX N-PSDB; ABN84610.
XX
XX Treatment and prevention of dental caries in mammals, in particular
XX humans by orally administering genetically engineered or purified
XX antibodies that bind to surface antigens of carcinogenic organisms.
XX
XX Claim 13; Fig 3A; 30pp; English.
XX

CC The present sequence is the protein sequence of the light chain variable
CC region (VL) of the murine monoclonal antibody SWLA3 (IGG), which binds
CC specifically to the surface antigens of carcinogenic type c Streptococcus

CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion
XX
XX Sequence 135 AA;

Query Match 91.6%; Score 630; DB 5; Length 135;
Best Local Similarity 92.4%; Pred. No. 7.9e-50;
Matches 122; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTQPLTSLVTIGQPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGDVVMTQPLTSLVTIGQPASISCKSSQSLDRDRTYLSWL 61
QY 61 LORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRVEADLGVYVCVQGTTHPPH 120
DB 62 LORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRVEADLGVYVCVQGTTHPP 121
QY 121 TFGGGTKLEIKR 132
DB 122 TFGGGTKLEIKR 133

RESULT 7
ADO00819
ID ADO00819 standard; protein; 133 AA.
XX
AC ADO00819;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antibody JRF/cAbeta40/10 light chain variable region, SEQ ID 6.
XX
KW Neuroprotective; Neurotropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW beta-amyloid-related disease; Alzheimer's disease; Abeta secretase;
KW cleavage site; immunogen; murine; antibody; light chain; variable region;
KW JRF/cAbeta40/10.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH Domain 44..59
FT /note= "CDR1"
FT Domain 75..81
FT /note= "CDR2"
FT Domain 114..122
FT /note= "CDR3"
XX WO2004029629-A1.
XX PN 08-APR-2004.
XX
XX 27-SEP-2002; 2002WO-EP011062.
XX
XX 27-SEP-2002; 2002WO-EP011062.
XX
XX (JANC) JANSSEN PHARM NV.
XX
XX Mercken MH, Vandermeeren MMP;
XX WPI: 2004-316180/29.
XX
XX New N-11 truncated amyloid-beta monoclonal antibodies specific for human
XX Amyloid-beta 11 N-terminal site (A-beta11-x peptides), useful for
XX diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's
XX disease.
XX

PS Disclosure; SEQ ID NO 6; 42pp; English.

XX The present invention relates to an antibody expressed by the hybridoma
 CC cells J6JPRD/hAbeta1/1 and J6JPRD/hAbeta1/2, which is capable of
 CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,
 CC Abeta11-x peptides). The antibody is useful for diagnosing beta-amyloid-
 CC related diseases. It is particularly useful for prognosing and monitoring
 CC response to therapy of Alzheimer's disease and other beta-amyloid related
 CC diseases and in passive immunization as a method for treating such
 CC diseases. A humanized form of the antibody is useful for manufacturing a
 CC medicament for treating, preventing or reversing cognitive decline in
 CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary
 CC Cerebral Hemorrhage with Amyloidosis of the Dutch Type, cerebral amyloid
 CC angiopathy or other beta-amyloid-related diseases, or to inhibit the
 CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta
 CC ; species in humans. It can also be used in assay systems such as
 CC competitive methods and nephelometry. The present sequence was used to
 CC illustrate the invention.

XX Sequence 133 AA;

XX Query Match 91.0%; Score 626; DB 8; Length 133;
 CC Best Local Similarity 90.9%; Pred. No. 1.8e-49;
 CC Matches 120; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLLYNGKTYLNL 60
 DB 2 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLLYNGKTYLNL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTPLTKISRVEADLGVYVCVQGTTHPPH 120
 DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTPLTKINRVEADLGVYVCVQGTTHPPH 121

QY 121 TFGGGTKLEIKR 132
 DB 122 TFGGGINLEIKR 133

RESULT 8
 ID ADO43845
 XX ADO43845 standard; protein; 133 AA.
 XX AC ADO43845;
 XX DT 15-JUL-2004 (first entry)
 XX DE Light chain variable region of anti-amyloid-beta antibody.
 XX KW antibody; Amyloid-beta1-x peptide; BACE-1; amyloid-beta; beta-secretase;
 KW beta-amyloid precursor protein; beta-amyloid-related disease;
 KW Alzheimer's disease; vaccine; Down's syndrome;
 KW hereditary cerebral haemorrhage; amyloidosis;
 KW cerebral amyloid angiopathy; amyloid plaque.

XX Mus sp.
 XX Key Location/Qualifiers
 FT Region 44..59
 FT /note= "CDR1"
 FT Region 75..81
 FT /note= "CDR2"
 FT Region 114..122
 FT /note= "CDR3"
 XX WO2004029630-A1.
 XX PD 08-APR-2004.
 XX PF 09-SEP-2003; 2003WO-EP010092.
 XX PR 27-SEP-2002; 2002WO-EP011062.
 XX PA (JANC) JANSSEN PHARM NV.

XX Mercken MH, Vandermeeren MMP; WPI; 2004-316181/29.
 XX New N-11 truncated amyloid-beta monoclonal antibodies specific for human
 PT Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing
 PT or treating beta-amyloid-related diseases e.g., Alzheimer's disease.
 XX Disclosure; Page 38-39; 50pp; English.

XX The specification describes a monoclonal antibody which specifically
 CC recognizes human Amyloid-beta1-x peptides. These peptides result from
 CC overexpression of BACE-1 which causes additional cleavage at the +11 site
 CC of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x
 CC peptides. BACE-1 is the major beta-secretase required for cleavage of
 CC beta-amyloid precursor protein. The antibody is useful for detecting the
 CC presence of amyloid-beta peptides in a tissue or fluid sample and for
 CC diagnosing beta-amyloid-related diseases. It is particularly useful for
 CC prognosing and monitoring response to therapy of Alzheimer's disease and
 CC other beta-amyloid related diseases and in passive immunization as a
 CC method for treating such diseases. A humanized form of the antibody is
 CC useful for manufacturing a medicament for treating, preventing or
 CC reversing cognitive decline in clinical or pre-clinical Alzheimer's
 CC Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with
 CC Amyloidosis of the Dutch type, cerebral amyloid angiopathy or other beta-
 CC amyloid-related diseases, or to inhibit the formation of amyloid plaques
 CC or the effects of toxic soluble Amyloid-beta species in humans. The
 CC present sequence represents the light chain variable region of an
 CC antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide
 CC amyloid-beta11-40.

XX Sequence 133 AA;

XX Query Match 91.0%; Score 626; DB 8; Length 133;
 CC Best Local Similarity 90.9%; Pred. No. 1.8e-49;
 CC Matches 120; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLLYNGKTYLNL 60
 DB 2 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLLYNGKTYLNL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTPLTKISRVEADLGVYVCVQGTTHPPH 120
 DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTPLTKINRVEADLGVYVCVQGTTHPPH 121

QY 121 TFGGGTKLEIKR 132
 DB 122 TFGGGINLEIKR 133

RESULT 9
 ID ABP58274
 XX ABP58274 standard; protein; 239 AA.
 XX AC ABP58274;
 XX DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX Humanised 3D6 antibody light chain.
 DE Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
 KW human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; neurotropic.
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= signal_peptide

Protein	21. .239	/label= Mature peptide	
FT	FT	/note= "the mature light chain is claimed in Claim 5"	
FT	FT	21. .133	
FT	FT	/note= "light chain variable region, claimed in Claim 4"	
FT	FT	44. .59	
FT	FT	/note= "CDR1"	
FT	FT	75. .81	
FT	FT	/note= "CDR2"	
FT	FT	114. .122	
FT	FT	/note= "CDR3"	
XX	XX		
PN	WO200288306-A2.		
XX	XX		
XX	07-NOV-2002.		
XX	XX		
XX	26-APR-2002; 2002WO-US011853.		
PF	PF		
XX	30-APR-2001; 2001US-0287539P.		
XX	XX		
PA	(ELIL) LILLY & CO ELI.		
PA	Tsurushita N, Vasquez M;		
PI			
XX	WPI; 2003-183835/18.		
DR	DR		
XX	N-PSDB; ABZ24632, ABZ24634.		
DR	DR		
XX	XX		
XX	New humanized forms of mouse 3D6 antibodies, useful for treating Down's		
PT	syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral		
PT	amyloid angiopathy, or for inhibiting formation of or reducing Abeta		
PT	plaque in the brain.		
XX	XX		
PS	Disclosure; Page 12-13; 54pp; English.		
XX	XX		
CC	The present sequence is that of a preferred light chain of a humanised		
CC	antibody of the present invention. In the variable region of this		
CC	sequence, the complementarity determining regions (CDRs) originate from		
CC	murine monoclonal antibody 3D6 and the framework region from human		
CC	germline V _k segment DPK19 and J segment JK4. Novel humanised antibodies		
CC	of the invention have CDRs from 3D6 and human framework sequences. These		
CC	humanised antibodies have binding affinities (affinity and epitope		
CC	location) approximately the same as those of the mouse 3D6 antibody. The		
CC	invention includes antibodies, single chain antibodies, and their		
CC	fragments, as well as nucleotide sequences, vectors, transformed host		
CC	cells, and methods of using the humanised antibody to treat, prevent,		
CC	alleviate, reverse or otherwise ameliorate symptoms and/or pathology		
CC	associated with Down's syndrome, (pre-)clinical Alzheimer's disease or		
CC	(pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or		
CC	reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise		
CC	OS field)		
XX	XX		
SQ	Sequence 239 AA;		
Query Match	90.1%; Score 620; DB 6; Length 239;		
Best Local Similarity	89.4%; Pred. No. 1.2e-48;		
Matches	118; Conservative 9; Mismatches 5; Indels 0; Gaps 0;		
Qy	1 MSPAQFLFLVLVLTQETNGDVVMTQPTPLTSLVTIGOPASISCKSSQSLLSYNGKTYLNLW 60		
Db	2 MSPAQFLFLVLVLTQETNGDVVMTQPTPLTSLVTIGOPASISCKSSQSLLSDSGKTYLNLW 61		
Qy	61 LQRFQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120		
Db	62 QQRFQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 121		
Qy	121 TFGGGTKLEIKR 132		
Db	122 TFGGGTKLEIKR 133		
RESULT 10			
AAR12361			
ID	AAR12361 standard; protein; 132 AA.		


```

AC AAR24712;
XX 25-MAR-2003 (revised)
DT '28-DEC-1992 (first entry)
XX
XX Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.
XX
XX Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= leader
FT Region 21..43
FT /label= Framework Region (FR) 1
FT Region 44..59
FT /label= complementarity determining region(CDR)1
FT Region 60..74
FT /label= FR-2
FT Region 75..81
FT /label= CDR-2
FT Region 82..112
FT /label= FR-3
FT Region 113..122
FT /label= CDR-3
FT Region 123..132
FT /label= FR-4
XX
XX EP491351-A2.
XX
XX 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-00121591.
XX
XX 18-DEC-1990; 90JP-00413829.
XX 11-NOV-1991; 91JP-00294464.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Tada H, Watanabe T;
XX
XX WPI; 1992-209528/26.
XX N-PSDB; AAQ25665.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
XX Example; Fig 1; 87pp; English.
XX
XX A genomic DNA library was prepd. from mouse anti-human fibrin specific
CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse
CC JK4-5 gene fragment as a hybridisation probe gave three positive
CC recombinant phage clones. Phage clone KE14 was identified as a clone
CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was
CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a
CC functional VK gene formed by recombination between the VK gene belonging
CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
XX Sequence 132 AA;
SQ
Query Match 88.4%; Score 608; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 8e-48;
Matches 119; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASISCKSSQSLLYSGKTYLNLW 60
DB 2 MSPAQFLFLVLWIRETNGDVVNAQTPLTSLVTIGOPAFISCKSSQSLSDSGKTYLNLW 61
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFFH 120

```

```

DB 62 LQRPQSPKRLIYLVSKLYSGVDPDRFTGSGSGTAFTLKINRVEAEDLGYYVCVQGTTHFFH 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132
XX
XX RESULT 14
XX ABG76931
ID ABG76931 standard; protein; 132 AA.
XX
XX AC ABG76931;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Humanised 3D6 light chain variable region #2.
XX
XX KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW notropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
XX OS Homo sapiens.
XX OS Mus musculus.
XX OS Synthetic.
XX
XX PN WO200246237-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 06-DEC-2001; 2001WO-US046587.
XX
XX PR 06-DEC-2000; 2000US-0251892P.
XX
XX PA (NEUR-) NEURALAB LTD.
XX
XX PA (AMHP ) WYETH.
XX
XX PI Basi G, Saldanha J, Yednock T;
XX
XX WPI; 2002-519658/55.
XX
XX Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
XX Claim 55; Page 157; 171pp; English.
XX
XX The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
XX Sequence 132 AA;
SQ
Query Match 87.4%; Score 601; DB 5; Length 132;
Best Local Similarity 87.8%; Pred. No. 3.5e-47;
Matches 115; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASISCKSSQSLLYSGKTYLNLW 60
DB 2 MSPAQFLFLVLWIRETNGDVVMTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLW 61
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCVQGTTHFFH 120

```

Db 62 LQKPGQSPQRLLIYLVSKLDSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYYCWOGTTHFPR 121

QY 121 TFGGQTKLEIK 131
||| |||: |||

Db 122 TFGGQTKVEIK 132

RESULT 15

ADR88415
ID ADR88415 standard; protein; 132 AA.

XX ADR88415;

XX 16-DEC-2004 (first entry)

XX Humanised 3D6 immunoglobulin light chain variable region SEQ ID NO:11.

XX 3D6; light chain variable region; immunoglobulin;

KW complementarity determining region; CDR; 10D5; variable framework region;

KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;

KW Alzheimer's disease.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..20 /label= signal peptide

FT Protein 21..132 /label= mature protein

XX WO2004080419-A2.

PN 23-SEP-2004.

XX 12-MAR-2004; 2004WO-US007503.

XX 12-MAR-2003; 2003US-00388389.

XX (NEUR-) NEURALAB LTD.

XX (AMHP) WYETH.

PI Basi G, Saldanha JW, Yednock T;

XX WPI; 2004-668880/65.

DR New humanized antibodies that recognize beta amyloid peptides, useful for

PT preventing or treating amyloidogenic diseases, such as Alzheimer's

PT disease.

XX Claim 55; SEQ ID NO 11; 176pp; English.

PS The invention relates to a novel humanised immunoglobulin light or heavy

CC chain. The humanised immunoglobulin light or heavy chain comprises:

CC variable region complementarity determining regions (CDR's) from the 3D6

CC immunoglobulin light chain variable region sequence of 132 amino acids

CC fully defined in the specification (ADR88406), or heavy chain variable

CC region sequence of 138 amino acids fully defined in the specification

CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region

CC sequence of 131 amino acids given in the specification (ADR88418) or

CC heavy chain variable region sequence of 142 amino acids fully defined in

CC the specification (ADR88420); and a variable framework region from a

CC human acceptor immunoglobulin light or heavy chain sequence, provided

CC that at least one framework residue is substituted with the corresponding

CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain

CC variable region sequence, where the framework residue is a residue that

CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR

CC -interacting residue or a residue participating in the VL-VH interface.

CC An antibody of the invention has neuroprotective and nootropic activity,

CC and may have a use in gene therapy. The composition and methods are

CC useful for preventing or treating an amyloidogenic disease, such as

CC Alzheimer's disease. The variable region sequence is useful in producing

CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin

CC chain, or its domain. The present sequence represents a humanised

CC immunoglobulin of the invention.

XX

SQ Sequence 132 AA;

Query Match 87.4%; Score 601; DB 8; Length 132;
Best Local Similarity 87.8%; Pred. No. 3.5e-47;
Matches 115; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLLYNGKTYLNL 60

Db 2 MSPAQFLFLVLVLTQETNGDVVMTQSPSLPVTPEPASISCKSSQSLDSDGKTYLNL 61

QY 61 LQKPGQSPQRLLIYLVSKLDSGVDPDRFTGSGSGGTDTFTLKISRVEAEDLGVYYCWOGTTHFPH 120

Db 62 LQKPGQSPQRLLIYLVSKLDSGVDPDRFSGSGSGGTDTFTLKISRVEAEDVGVYYCWOGTTHFPR 121

QY 121 TFGGQTKLEIK 131

Db 122 TFGGQTKVEIK 132

Search completed: May 25, 2005, 15:47:18
Job time : 64.1321 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-11
Perfect score: 688
Sequence: 1 MSPAQFLFLVLVLTQETNGD.....VOGTHPHTFGGTYKLEIKR 132

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	91.7	131	4	US-09-647-468-163
2	628	91.3	131	4	US-09-647-468-164
3	596	86.6	142	4	US-09-840-459-102
4	596	86.6	142	4	US-09-497-625A-102
5	555	80.7	132	1	US-08-477-877B-91
6	555	80.7	132	2	US-08-472-281A-91
7	555	80.7	132	2	US-08-477-989B-91
8	555	80.7	257	4	US-09-419-788-113
9	553	80.4	113	4	US-09-698-705-7
10	553	80.4	218	4	US-09-698-705-12
11	546	79.4	112	4	US-09-809-739-11
12	546	79.4	112	4	US-09-840-459-9
13	546	79.4	112	4	US-09-497-625A-9
14	542	78.8	112	4	US-09-647-468-149
15	542	78.8	112	4	US-09-647-468-150
16	541	78.6	353	4	US-09-203-958A-4
17	537	78.1	112	4	US-09-840-459-54
18	537	78.1	112	4	US-09-497-625A-54
19	536	77.9	132	1	US-08-477-877B-84
20	536	77.9	132	2	US-08-472-281A-84
21	536	77.9	132	2	US-08-477-989B-84
22	534	77.6	535	3	US-08-983-035A-38
23	527	76.6	112	2	US-08-678-194-6
24	527	76.6	112	3	US-08-890-011-6
25	527	76.6	112	3	US-09-262-724-6
26	524	76.2	112	3	US-09-184-658-49
27	524	76.2	112	4	US-09-504-262D-49

28	524	76.2	112	4	US-09-809-739-16	Sequence 16, Appl
29	524	76.2	112	4	US-09-840-459-14	Sequence 14, Appl
30	524	76.2	112	4	US-09-497-625A-14	Sequence 14, Appl
31	524	76.2	242	4	US-09-479-614-20	Sequence 20, Appl
32	522	75.9	135	1	US-08-259-372A-12	Sequence 12, Appl
33	522	75.9	135	1	US-08-468-671-12	Sequence 12, Appl
34	521	75.7	289	3	US-03-184-658-63	Sequence 63, Appl
35	521	75.7	289	4	US-09-504-262D-63	Sequence 63, Appl
36	520	75.6	113	3	US-09-214-095D-116	Sequence 116, App
37	519	75.4	100	4	US-09-840-459-23	Sequence 23, Appl
38	519	75.4	100	4	US-09-497-625A-23	Sequence 23, Appl
39	519	75.4	112	4	US-09-809-739-17	Sequence 17, Appl
40	519	75.4	112	4	US-09-840-459-15	Sequence 15, Appl
41	519	75.4	112	4	US-09-497-625A-15	Sequence 15, Appl
42	516	75.0	112	4	US-09-809-739-15	Sequence 15, Appl
43	516	75.0	112	4	US-09-840-459-13	Sequence 13, Appl
44	516	75.0	112	4	US-09-497-625A-13	Sequence 13, Appl
45	511	74.3	112	4	US-09-809-739-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-647-468-163
; Sequence 163, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAHITO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163

Query Match 91.7%; Score 631; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 2.8e-53;
Matches 122; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTTSVTIGQPASICKSSQSLYNGKTYLNWL 60
DB 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTTSVTIGQPASICKSSQSLYNGKTYLNWL 60
QY 61 LQRPQSPKRLIYLVSKLDSCGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120
DB 61 LQRPQSPKRLIYLVSKLDSCGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPD 120
QY 121 TFGGTYKLEIK 131
DB 121 TFGGTYKLEIK 131

RESULT 2

US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOKIHO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 164
LENGTH: 131
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for L chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody A1R-8
US-09-647-468-164

Query Match 91.3%; Score 628; DB 4; Length 131;
Best Local Similarity 92.4%; Pred. No. 5 4e-53;
Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLMQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWL 60
DB 1 MSPAQFLFLVLMQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWL 60
QY 61 LQPPGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPH 120
DB 61 LQPPGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPH 120
QY 121 TFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 3
US-09-840-459-102
Sequence 102, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 102
LENGTH: 142
TYPE: PRT
ORGANISM: Mus musculus
US-09-840-459-102

Query Match 86.6%; Score 596; DB 4; Length 142;
Best Local Similarity 92.7%; Pred. No. 7e-50;
Matches 115; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 9 LVLVMIQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 68
DB 7 LVLVMIQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 66
QY 69 KELIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPHFTFGGTKL 128
DB 67 KELIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPHFTFGGTKL 126
QY 129 EIKR 132
DB 127 EIKR 130

RESULT 4
US-09-497-625A-102
Sequence 102, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 102
LENGTH: 142
TYPE: PRT
ORGANISM: Mus musculus
US-09-497-625A-102

Query Match 86.6%; Score 596; DB 4; Length 142;
Best Local Similarity 92.7%; Pred. No. 7e-50;
Matches 115; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 9 LVLVMIQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 68
DB 7 LVLVMIQETNGDVMTQTPLTSLVTIGOPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 66
QY 69 KELIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPHFTFGGTKL 128
DB 67 KELIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTFFPHFTFGGTKL 126
QY 129 EIKR 132
DB 127 EIKR 130

RESULT 5
US-08-477-877B-91
Sequence 91, Application US/0847787B
Patent No. 5730979
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:


```

COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Humanized LO-CD2a light chain variable region.
US-08-472-281A-91

Query Match      80.7%; Score 555; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 5.5e-46;
Matches 106; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY      1 MSPAPFLFLVLWLIQETNGDVVMTQPTPLTSVTIGOPASISCKSSQSLLYSNGKTYLNWL 60
DB      2 MSPVQSLFLLLWLILGTNGDVVMTQSPPLSLVTLGQPASISCKSSQSLHSSGNTLYNL 61

QY      61 LQRPQSPKRLIYLVSKDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVGYVCVQGTFFPH 120
DB      62 LQRPQSPQPLIYLVSKLESGVDPDRFSGSGSGTDFTLKISGVEAEDVGYYCNCQFTHPY 121

QY      121 TFGGGTKLEIK 131
DB      122 TFGQGTKEIK 132

RESULT 7
US-08-477-989B-91
; Sequence 91, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road

```

```
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain
; NAME/KEY: variable region.
;
US-08-477-989B-91

Query Match 80.7%; Score 555; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 5.5e-46;
Matches 106; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIQIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
Db 2 MSPVQSLFLILLILCTNGDVVMTQPSLLVTLGQPASISCKSSQSLHSSGNTYLNWL 61
QY 61 LQRPQSPKRLIYLVSKLSDGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPH 120
Db 62 LQRPQSPQLIYLVSKLSSGVPDRFSGSGSGTDTFLKISGVAEADVGYYVCQFTFPHY 121
QY 121 TFGGTTKLEIK 131
Db 122 TFGGTTKLEIK 132

RESULT 8
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189p

; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain
; NAME/KEY: variable region.
;
US-08-477-989B-91

Query Match 80.7%; Score 555; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 5.5e-46;
Matches 106; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIQIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
Db 2 MSPVQSLFLILLILCTNGDVVMTQPSLLVTLGQPASISCKSSQSLHSSGNTYLNWL 61
QY 61 LQRPQSPKRLIYLVSKLSDGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPH 120
Db 62 LQRPQSPQLIYLVSKLSSGVPDRFSGSGSGTDTFLKISGVAEADVGYYVCQFTFPHY 121
QY 121 TFGGTTKLEIK 131
Db 122 TFGGTTKLEIK 132

RESULT 8
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189p

; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
;
US-09-419-788-113

Query Match 80.7%; Score 555; DB 4; Length 257;
Best Local Similarity 94.7%; Pred. No. 1.2e-45;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTSLVTTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 137 DVLMTQAPLTLTSLVTTIGQPASISCKSSQSLDGDGKTYLNWLLQRPQSPKRLIYLVSKLD 196
QY 80 SGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPHFTGGTTKLEIKR 132
Db 197 SGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPHFTGGTTKLEIKR 249

RESULT 9
US-09-698-705-7
; Sequence 7, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
;
US-09-698-705-7

Query Match 80.4%; Score 553; DB 4; Length 113;
Best Local Similarity 95.6%; Pred. No. 7.2e-46;
Matches 108; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTSLVTTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQTPLTSLVTTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSTLD 60
QY 80 SGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPHFTGGTTKLEIKR 132
Db 61 SGVPDRFTGSGSGTDTFLKISRVEAEDLGYYVCVQGTFFPHFTGGTTKLEIKR 113

RESULT 10
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
```

```
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177781
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      80.4%; Score 553; DB 4; Length 218;
Best Local Similarity 95.6%; Pred. No. 1.6e-45;
Matches 108; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 20 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIKR 132
Db 61 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIKR 113

RESULT 11
US-09-809-739-11
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match      79.4%; Score 546; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-45;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 20 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIKR 131
Db 61 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIKR 112

RESULT 13
US-09-497-625A-9
; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
```

```
Qy 20 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIK 131
Db 61 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIK 112

RESULT 12
US-09-840-459-9
; Sequence 9, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-9

Query Match      79.4%; Score 546; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-45;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 20 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVMTQTPLTSLVSTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIK 131
Db 61 SGVPRFTGSGSGTDTLTKISRVEADLGVVYCVQGTFFPHTFGGTTKLEIK 112

RESULT 13
US-09-497-625A-9
; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
```

```
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match          78.8%; Score 542; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 8.1e-45;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVLTQTPLTLSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60

QY 80 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPFTFGGGTKLEIK 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCWQDTHFPDFTFGGGTKLEIK 112

Search completed: May 25, 2005, 15:58:24
Job time : 17.454 secs

; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match          78.8%; Score 542; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 8.1e-45;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVLTQTPLTLSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60

QY 80 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPFTFGGGTKLEIK 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCWQDTHFPDFTFGGGTKLEIK 112

Search completed: May 25, 2005, 15:58:24
Job time : 17.454 secs

; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match          78.8%; Score 542; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 8.1e-45;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVLTQTPLTLSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60

QY 80 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPFTFGGGTKLEIK 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCWQGTTHPFTFGGGTKLEIK 112

RESULT 14
US-09-647-468-149
; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NACHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match          78.8%; Score 542; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 8.1e-45;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVLTQTPLTLSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60

QY 80 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPFTFGGGTKLEIK 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYVCWQDTHFPDFTFGGGTKLEIK 112

RESULT 15
US-09-647-468-150
; Sequence 150, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NACHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773A-11
Perfect score: 688
Sequence: 1 MSPAQFLFLVLWLTQETNGD.....VQGTHTFHTFGGTTKLEIKR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	100.0	132	13	US-10-006-773-11
2	636	92.4	132	14	US-10-010-942B-2
3	636	92.4	132	15	US-10-388-389-2
4	636	92.4	132	16	US-10-703-713-2
5	636	92.4	132	16	US-10-704-070-2
6	636	92.4	132	17	US-10-232-030-2
7	631	91.7	131	15	US-10-462-062-163
8	630	91.6	135	9	US-09-881-823-10
9	628	91.3	131	15	US-10-462-062-164
10	620	90.1	239	17	US-10-476-265-19
11	606	88.1	145	17	US-10-861-662-52
12	606	88.1	145	17	US-10-861-662-58
13	606	88.1	145	17	US-10-861-662-61

14	601	87.4	132	14	US-10-010-942B-11	Sequence 11, Appl
15	601	87.4	132	15	US-10-388-389-11	Sequence 11, Appl
16	601	87.4	132	16	US-10-703-713-11	Sequence 11, Appl
17	601	87.4	132	16	US-10-704-070-11	Sequence 11, Appl
18	601	87.4	132	17	US-10-232-030-11	Sequence 11, Appl
19	596	86.6	142	9	US-09-840-459-102	Sequence 102, App
20	596	86.6	142	16	US-10-766-773-102	Sequence 102, App
21	596	86.6	142	16	US-10-766-610-102	Sequence 102, App
22	596	86.6	142	16	US-10-733-563-102	Sequence 5, Appl
23	592	86.0	132	14	US-10-010-942B-5	Sequence 5, Appl
24	592	86.0	132	15	US-10-388-389-5	Sequence 5, Appl
25	592	86.0	132	15	US-10-703-713-5	Sequence 5, Appl
26	592	86.0	132	16	US-10-704-070-5	Sequence 5, Appl
27	592	86.0	132	17	US-10-232-030-5	Sequence 7, Appl
28	553	80.4	113	17	US-10-937-046-7	Sequence 5, Appl
29	553	80.4	218	17	US-10-937-046-12	Sequence 12, Appl
30	552	80.2	122	15	US-10-272-899A-86	Sequence 86, Appl
31	552	80.2	130	15	US-10-272-899A-88	Sequence 88, Appl
32	546	79.4	112	9	US-09-835-087-1	Sequence 1, Appl
33	546	79.4	112	9	US-09-809-739-11	Sequence 11, Appl
34	546	79.4	112	9	US-09-840-459-9	Sequence 9, Appl
35	546	79.4	112	16	US-10-766-773-9	Sequence 9, Appl
36	546	79.4	112	16	US-10-766-610-9	Sequence 9, Appl
37	546	79.4	112	16	US-10-733-563-9	Sequence 9, Appl
38	542	78.8	112	15	US-10-462-062-149	Sequence 149, App
39	542	78.8	112	15	US-10-462-062-150	Sequence 150, App
40	541	78.6	112	17	US-10-855-013-12	Sequence 12, Appl
41	541	78.6	353	10	US-09-203-958A-4	Sequence 4, Appl
42	539	78.3	162	15	US-10-410-907A-30	Sequence 30, Appl
43	539	78.3	500	14	US-10-168-809-22	Sequence 22, Appl
44	537	78.1	112	9	US-09-840-459-54	Sequence 54, Appl
45	537	78.1	112	16	US-10-766-773-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-006-773-11
; Sequence 11, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-11

Query Match	100.0%	Score 688;	DB 13;	Length 132;
Best Local Similarity	100.0%	Pred. No. 1.6e-54;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSPAQFLFLVLWLTQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYNGKTYLNLW	60	
Db	1	MSPAQFLFLVLWLTQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYNGKTYLNLW	60	
Qy	61	LQRQSPKRLIYLVSKLDCVDPDRFTGSGSGTDTLTKISRVEADLGVYVCVQGTTHPPH	120	
Db	61	LQRQSPKRLIYLVSKLDCVDPDRFTGSGSGTDTLTKISRVEADLGVYVCVQGTTHPPH	120	
Qy	121	TFGGGTKEIKR	132	
Db	121	TFGGGTKEIKR	132	

```
RESULT 2
US-10-010-942B-2
; Sequence 2, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2

Query Match          92.4%; Score 636; DB 14; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGVYVMTQPTLTLSVTIGOPASISCKSSQSLDSGKTYLNL 61
QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 120
DB 62 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 3
US-10-388-389-2
; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

Query Match          92.4%; Score 636; DB 15; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGVYVMTQPTLTLSVTIGOPASISCKSSQSLDSGKTYLNL 61
QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 120
DB 62 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 4
US-10-703-713-2
; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2

Query Match          92.4%; Score 636; DB 16; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGVYVMTQPTLTLSVTIGOPASISCKSSQSLDSGKTYLNL 61
QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 120
DB 62 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 5
US-10-704-070-2
; Sequence 2, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

Query Match          92.4%; Score 636; DB 15; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNL 60
DB 2 MSPAQFLFLVLWIRETNGVYVMTQPTLTLSVTIGOPASISCKSSQSLDSGKTYLNL 61
QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 120
DB 62 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLVVYVCVQGTFFPH 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132
```

```

; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

Query Match          92.4%; Score 636; DB 16; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSPAQFLFLVLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYNGKTYLNL 60
Db 2 MSPAQFLFLVLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYNGKTYLNL 61
Qy 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120
Db 62 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 121
Qy 121 TFGGGTKLEIK 131
Db 122 TFGGGTKLEIK 132

RESULT 7
US-10-462-062-163
; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163

Query Match          91.7%; Score 631; DB 15; Length 131;
Best Local Similarity 93.1%; Pred. No. 2.2e-49;
Matches 122; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSPAQFLFLVLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYNGKTYLNL 60
Db 1 MSPAQFLFLVLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYNGKTYLNL 60
Qy 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120
Db 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120
Qy 121 TFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 8
US-09-881-823-10
; Sequence 10, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
```



```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-662-52

Query Match      88.1%; Score 606; DB 17; Length 145;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 68
Db 14 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 73

Qy 69 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 128
Db 74 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 133

Qy 129 EIKR 132
Db 134 EIKR 137

RESULT 12
US-10-861-662-58
; Sequence 58, Application US/10861662
; Publication No. US20050086707A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etesami, Soudabeh
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Paris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/861,662
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-662-58

Query Match      88.1%; Score 606; DB 17; Length 145;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 68
Db 14 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 73

Qy 69 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 128
Db 74 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 133

Qy 129 EIKR 132
Db 134 EIKR 137

RESULT 13
US-10-861-662-61
; Sequence 61, Application US/10861662
; Publication No. US20050086707A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etesami, Soudabeh
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Paris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/861,662
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-662-61

Query Match      88.1%; Score 606; DB 17; Length 145;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 68
Db 14 LVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSSQSLYSNGKTYLNMLLQRPQSP 73

Qy 69 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 128
Db 74 KRLIYLVSKLDGVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTTHPFTFGGTKL 133

Qy 129 EIKR 132
Db 134 EIKR 137

RESULT 14
US-10-010-942B-11
; Sequence 11, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
```

```
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-11
```

```
Query Match      87.4%; Score 601; DB 14; Length 132;
Best Local Similarity 87.8%; Pred. No. 1.2e-46;
Matches 115; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNWL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 MSPAQFLFLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLDSDGKTYLNWL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHPPH 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 LQPGQSPQRLIYLVSKLDSGVDPDRFSGSGGTDFTLKISRVEAEDVGVIYCVQGTTHPPR 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TFGGGTKLEIK 131
   |||||:|||||
Db 122 TFGGGTKVEIK 132
   |||||:|||||
```

```
RESULT 15
US-10-388-389-11
; Sequence 11, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Vedrock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-11
```

```
Query Match      87.4%; Score 601; DB 15; Length 132;
Best Local Similarity 87.8%; Pred. No. 1.2e-46;
Matches 115; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNWL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 MSPAQFLFLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLDSDGKTYLNWL 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LQPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHPPH 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 LQPGQSPQRLIYLVSKLDSGVDPDRFSGSGGTDFTLKISRVEAEDVGVIYCVQGTTHPPR 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TFGGGTKLEIK 131
   |||||:|||||
```

```
Db 122 TFGGGTKVEIK 132
   |||||:|||||

Search completed: May 25, 2005, 16:06:51
Job time : 61.0292 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773A-11
Perfect score: 688
Sequence: 1 MSPAQFLFLVLVWVQETNGD.....VQGTHTFPGGTTKLEIKR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	94.3	132	2 C32513	Ig kappa chain pre
2	603	87.6	131	2 S31577	Ig kappa chain - m
3	569	82.7	112	2 P10273	Ig kappa chain V r
4	561	81.5	113	2 P10560	Ig kappa chain V r
5	547	79.5	112	2 A55491	proteolytic antibo
6	543	78.9	133	2 S23230	Ig kappa chain pre
7	540	78.5	111	2 S20709	Ig kappa chain V r
8	538	78.2	133	2 S40324	Ig kappa chain V r
9	533	77.5	133	1 K2HURP	Ig kappa chain pre
10	532	77.3	133	2 S42611	HUNK protein prec
11	531	77.2	112	2 A36259	Ig kappa chain V r
12	527	76.6	142	2 S22902	Ig kappa chain V r
13	521	75.7	133	1 A24452	Ig kappa chain pre
14	515	74.9	132	2 S40322	Ig kappa chain - h
15	513.5	74.6	140	2 S22658	Ig kappa chain pre
16	505	73.4	101	2 A37330	Ig kappa chain V r
17	501	72.8	103	2 P11055	Ig kappa chain V r
18	492	71.5	120	2 S42267	Ig kappa chain V r
19	489	71.1	103	2 P11056	Ig kappa chain V r
20	488	70.9	128	2 S40373	Ig kappa chain - h
21	488	70.7	114	2 S49572	Ig kappa chain pre
22	486.5	70.6	126	2 S40312	Ig kappa chain - h
23	486	70.6	131	2 D29380	Ig kappa chain pre
24	486	70.6	136	2 S40357	Ig kappa chain V-J
25	485	70.5	118	2 S40374	Ig kappa chain - h
26	485	70.5	132	2 S26882	Ig kappa chain V r
27	483	70.2	132	2 B34904	Ig kappa chain pre
28	482	70.1	131	2 S09259	Ig kappa chain pre
29	481	69.9	131	2 S09259	Ig kappa chain pre

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C:Accession: C32513

R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and

A:Reference number: A94689; MUID:88331394; PMID:3138286

A:Accession: C32513

A:Molecule type: DNA

A:Residues: 1-132 <KOF>

A:Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 94.3%; Score 649; DB 2; Length 132;
Best Local Similarity 96.2%; Pred. No. 2.2e-48;
Matches 126; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MSPAQFLFLVLVWVQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLNSGKTYLNLW 60
Db	1	
Qy	61	LQRFQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 120
Db	62	LQRFQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 121
Qy	121	TFGGGTKEIK 131
Db	122	TFGGGTKEIK 132

RESULT 2

S31577

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S31577

R:Reinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A:Description: Immunoglobulin variable heavy and light chain cDNA sequences for two anti

A:Reference number: S31577

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <REC>

A:Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 603; DB 2; Length 131;
Best Local Similarity 88.5%; Pred. No. 1.8e-44;
Matches 116; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLVWQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWL 60
Db 1 MSPAQFLFLVLVWQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWL 60
QY 61 LQPGQSPKRLIYLVSKLSDGVPDRFTGSGSDHFTLKISRVEADLGYYVCVQGTTHFP 120
Db 61 LQPGQSPKRLIYLVSKLSDGVPDRFTGSGSDHFTLKISRVEADLGYYVCVQGTTHFP 120
QY 121 TFGGGTKLEIK 131
Db 121 TFGGGTKLEWK 131

RESULT 3
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: PL0273
J:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0273
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
A:Cross-references: UNIPROT:Q8K0F8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
F;55-61/Region: complementarity-determining 2
F;62-93/Region: framework 3
F;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match 82.7%; Score 569; DB 2; Length 112;
Best Local Similarity 98.2%; Pred. No. 1.2e-41;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 80 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIK 131
Db 61 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIK 112

RESULT 4
F30560
Ig kappa chain V region (28.4.10A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: F30560
R:Watsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal
A:Reference number: A30560; MUID:89110062; PMID:2464028
A:Accession: F30560
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <WAT>
A:Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 561; DB 2; Length 113;
Best Local Similarity 96.5%; Pred. No. 5.8e-41;
Matches 109; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 20 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 80 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIKR 132
Db 61 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIKR 113

RESULT 5
A55491
proteolytic antibody light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55491
J:Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R
J. Biol. Chem. 269, 32389-32393, 1994
A:Title: Molecular cloning of a proteolytic antibody light chain.
A:Reference number: A55491; MUID:95096089; PMID:7798238
A:Accession: A55491
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <GAO>
A:Cross-references: UNIPROT:Q8K0F8; GB:L34775
A:Note: authors translated the codon TAT for residue 37 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 547; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 8.9e-40;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 20 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQPTLTLSVTIGQPASISCKSSQSLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
QY 80 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIK 131
Db 61 SGVPDRFTGSGSDTFTLKISRVEADLGYYVCVQGTTHFPHTFGGTTKLEIK 112

RESULT 6
S23230
Ig kappa chain precursor V-J region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S23230
R:Kennedy, M.A.
J. Exp. Med. 173, 1033-1036, 1991
A:Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light
A:Reference number: S23230; MUID:91178438; PMID:1840606
A:Accession: S23230
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KEN>
A:Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
C:Genetics:
A:Introns: 17/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
Query Match 78.9%; Score 543; DB 2; Length 133;
Best Local Similarity 77.7%; Pred. No. 2.3e-39;
Matches 101; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

```

QY 3 PAQFLPLLVLWIOETNGDVVMTPTLTLSVTIGQPASISCKSSQSLYSNGKTYIANWLQ 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 PAQLGLLLMLWVPGSSGDVVMTQSPUSPLVTLTGQPASISCRSSQSLYSVSGNTHLWFOQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 RPQSQPKRLIYLSKLDGVPDRFTGSGSGDFTLKLISRVEADLGVVYVCVQGTTHPHTF 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 RPQSPRLIYKSNRDSGVDRFSGSGSGDFTLKLISRVEADGVVYCMQGTTHPPTF 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 123 GGGTKLEIKR 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 GGGTKLEIKR 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
S20709
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20709
R:Brennand, D.M.; Hands, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osb
submitted to the EMBL Data Library, April 1992
A:Description: Binding specificity and variable region sequences of two monoclonal antib
A:Reference number: S20706
A:Accession: S20709
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <BRE>
A:Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMW>

Query Match 78.5%; Score 50; DB 2; Length 111;
Best Local Similarity 92.8%; Pred. No. 3.5e-39;
Matches 103; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 20 DVVMTPTLTLSVTIGQPASISCKSSQSLYSNGKTYIANWLQPGSQPKRLIYLSKLD 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIQLTQSPLTLSVTIGQPASISCKSSQSLHSDGKTYIANWLQPGSQPKRLIYLSKLD 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 SGVPDRFTGSGSGDFTLKLISRVEADLGVVYVCVQGTTHPHTFGGTTKLEI 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 SGVPDRFTGSGSGDFTLKLISRVEADLGVVYVCVQGTTHPHTFGGTTKLEI 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 8
S40324
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8256341
A:Accession: S40324
A:Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: UNIPROT:Q87CD0; EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMW>

```

```

Query Match      78.2%; Score 538; DB 2; Length 133;
Best Local Similarity 76.9%; Pred. No. 6.2e-3;
Matches 100; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 3 PAQFLFLVLVIQETNGDDVYMTQPTLSVTIGQPASISCKSQSLYSNGKTYLNVLLQ 62
      ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1 PAQLLGILLMLVPGSSGDVLTQSPFLPVTLGQPASISCRDQSLVYSDGKTYLVNYYQ 60
      ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

```

```

Qy 63  RQSGPRRLLYLVSKLDSGVDPDRFTSGSGCTDFTLKLSRVEADLGVVYCVQGTHERPTF 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61  RQSGPRRLLYKVSNRDSGVDPDRFTSGSGCTDFTLISRVEADGVVYCMQGTHTPGTF 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 123  GGGTKLEIKR 132
      |||||:|||||
Db 121  GQGTKVBIKR 130
      |||||:|||||

RESULT 9
K2HURP
Ig kappa chain precursor V-II region (RPMI) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combiato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06310
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:I36265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical
      chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associat
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/disulfide bonds: #status predicted

```

Query Match	77.5%;	Score 533;	DB 1;	Length 133;
Best Local Similarity	76.9%;	Pred. No. 1.6e-38;		
Matches 100;	Conservative 16;	Mismatches 14;	Indels 0;	Gaps 0
Qy	3	PAQFLFLVLLWIGETNGDVVMTQPTPLTSVITIGOPASTSCSSOSLLYSGNGKTYLNLLQ	62	
Db	4	PAQLGLLMLWPGSSGDVVMTQPLSLPVLTLGPASPISCRSSOSLVYSDGNTYLNWFPQ	63	
Qy	63	RPQSPKRLIYLVSKDSGVPDRFTGSGSGTDFTFLKISRVEAEDLVGYCYVQGTFFPHTF	122	
Db	64	RPQSPRLIYKVSNRDSGVDPDRSGSGSGTDFTFLKISRVEAEDLVGYCYVQGTHTSWTF	123	
Qy	123	GGGTKLEIKR	132	
Db	124	GGGTKVEIKR	133	

RESULT 10
S42611
HUNKV protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S42611
R:Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A:title: DNA sequence analysis and comparison of the variable heavy and light
A:Reference number: S42610; MUID:92138794; PMID:1370957
A:Accession: S42611

Search completed: May 25, 2005, 16:48:39
Job time : 19.6642 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.3423 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773A-11

Perfect score: 688

Sequence: 1 MSPAQFLFLVWVQETNGD.....VOGTHPHTFGGTYKLEIKR 132

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	77.8	239	2 Q8TCD0	Q8tcd0 homo sapien
2	533	77.5	133	1 KV2F HUMAN	P06310 homo sapien
3	495	71.9	239	2 Q6P491	Q6p491 homo sapien
4	485	70.5	239	2 Q8NEK0	Q8nek0 homo sapien
5	472.5	68.7	240	2 Q6PIH6	Q6pih6 homo sapien
6	466.5	67.8	114	2 Q9UL80	Q9ul80 homo sapien
7	456	66.3	113	1 KV2G MOUSE	P01631 mus musculus
8	450	65.4	219	2 Q65ZC0	Q65zc0 mus musculus
9	444	64.5	113	1 KV2B HUMAN	P01615 homo sapien
10	444	64.5	117	1 KV2E HUMAN	P06309 homo sapien
11	443	64.4	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
12	430	62.5	113	1 KV2D HUMAN	P01617 homo sapien
13	421.5	61.3	115	1 KV2A HUMAN	P01630 mus sapien
14	417	60.6	113	1 KV2F HUMAN	P01630 mus sapien
15	412	59.9	112	2 Q6LEM8	Q6lem8 mus musculus
16	410	59.6	113	1 KV2E MOUSE	P03976 mus musculus
17	401.5	58.4	112	1 KV2C HUMAN	P01616 homo sapien
18	399	58.0	133	1 KV4B HUMAN	P06313 homo sapien
19	397.5	57.8	134	1 KV4C HUMAN	P06314 homo sapien
20	392	57.0	113	1 KV2C MOUSE	P01628 mus musculus
21	392	57.0	120	1 KV2B MOUSE	P01627 mus musculus
22	391	56.8	112	1 KV2D MOUSE	P01629 mus musculus
23	389	56.5	129	1 KV3L HUMAN	P18135 homo sapien
24	385.5	56.0	236	2 Q6PIL8	Q6pil8 homo sapien
25	383	55.7	112	1 KV2A MOUSE	P01626 mus musculus
26	382	55.5	129	1 KV3M HUMAN	P18136 homo sapien
27	380	55.2	235	2 Q6GMV9	Q6gmv9 homo sapien
28	375.5	54.6	108	1 KV1 CANFA	P01618 canis famil
29	374.5	54.4	236	2 Q6P5S8	Q6p5s8 homo sapien
30	372.5	54.1	114	1 KV4A HUMAN	P01625 homo sapien
31	371.5	54.0	111	1 KV3L MOUSE	P01664 mus musculus

RESULT 1

ID	Q8TCD0	PRELIMINARY;	PRT;	239 AA.
AC	Q8TCD0;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
EX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RA	Strausberg R.			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC022362; AAH22362.1; -			
DR	PIR; S22658; S22658.			
DR	PIR; S34095; S34095.			
DR	PIR; S40324; S40324.			
DR	PIR; S40374; S40374.			
DR	PIR; S42267; S42267.			
DR	PIR; S42268; S42268.			
DR	HSSP; P01834; I17Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_cl.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF07654; C1-set; I.			

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein_unknwn_1.
 SQ SEQUENCE 239 AA; 26234 MW; 5133CAAF3673009EE CRC64;
 Query Match 77.8%; Score 535; DB 2; Length 239;
 Best Local Similarity 76.2%; Pred. No. 2.5e-44;
 Matches 99; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
 QY 3 PAQFLFLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLYNGKTYLNWLLQ 62
 DB 4 PAQLGLLMLWPGSSGDVVMTPQSLPLPVTIGQPASISCRSSQSLVSDGNTYLNWFOQ 63
 QY 63 RQSQPKRLIYLVSKLDGVPDRFTGSGSGTDTFLKISRVEAEDLGVCYVCGTHPPHPTF 122
 DB 64 RQSQPRRLIYKVNRDVGVPDRFSGSGSGTDTFLKISRVEAEDLGVCYVCGTHPPSTP 123
 QY 123 GGGTKLEIKR 132
 DB 124 GGGTKLEIKR 133
 RESULT 2
 KV2F HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobek H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and III."
 RL Nucleic Acids Res. 13:6499-6513 (1985).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z00020; CAA77315.1; --
 DR FIR; A01890; K2HURP.
 DR HSP; Q99M37; 1191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 59 Complementarity-determining-1.
 FT DOMAIN 60 74 Framework-2.
 FT DOMAIN 75 81 Complementarity-determining-2.
 FT DOMAIN 82 113 Framework-3.
 FT DOMAIN 114 122 Complementarity-determining-3.
 FT DOMAIN 123 132 Framework-4.
 FT DISULFID 43 113 By similarity.

FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14707 MW; 5133CAAF3673009EE CRC64;
 Query Match 77.5%; Score 533; DB 1; Length 133;
 Best Local Similarity 76.9%; Pred. No. 2e-44; Indels 0; Gaps 0;
 Matches 100; Conservative 16; Mismatches 14;
 QY 3 PAQFLFLVLTQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLYNGKTYLNWLLQ 62
 DB 4 PAQLGLLMLWPGSSGDVVMTPQSLPLPVTIGQPASISCRSSQSLVSDGNTYLNWFOQ 63
 QY 63 RQSQPKRLIYLVSKLDGVPDRFTGSGSGTDTFLKISRVEAEDLGVCYVCGTHPPHPTF 122
 DB 64 RQSQPRRLIYKVNRDVGVPDRFSGSGSGTDTFLKISRVEAEDLGVCYVCGTHPPSTP 123
 QY 123 GGGTKLEIKR 132
 DB 124 GGGTKVEIKR 133
 RESULT 3
 Q6P491 PRELIMINARY; PRT; 239 AA.
 ID Q6P491;
 AC Q6P491;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063599; AAH63599.1; --
 DR HSP; P01837; 1KCU
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.

[illegible]


```
RT allergen Chi t I.";  
RL Int. Arch. Allergy Immunol. 110:348-353(1996).  
DR EMBL; Z37499; CAA85724.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.  
FT NON_TER 1  
FT NON_TER 219  
SQ SEQUENCE 219 AA; 23944 MW; 7E1B92A14EAF8445 CRC64;  
  
Query Match 65.4%; Score 450; DB 2; Length 219;  
Best Local Similarity 75.2%; Pred. No. 5.1e-36;  
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;  
  
QY 20 DVNMTQPLTSLVITGQPASISCKSSQSLLYSNKTYLNWLLQRPQSPKRLIYLVSKLD 79  
Db 1 ELVMTQSPLSVSLGDAQSISCRSSQSLVHTNGNTYLNWLLQRPQSPKRLIYLVSKLD 79  
QY 80 SGVPDRFTGSGSDTFTLKISRVEAEDLGVCYVCGVTHPHTFGGTTKLEIKR 132  
Db 61 SGVPDRFTGSGSDTFTLKISRVEAEDLGVCYVCGVTHPHTFGGTTKLEIKR 113  
  
RESULT 9  
KV2B HUMAN  
ID KV2B HUMAN STANDARD; PRT; 113 AA.  
AC P01615;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region FR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76253627; PubMed=821524;  
RA Riesen W.F., Jaton J.-C.;  
RT "Variable region sequence of the light chain from a Waldenstroms IgM  
with specificity for phosphorylcholine.";  
RL Biochemistry 15:3829-3833(1976).  
CC -I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's  
macroglobulin that binds phosphorylcholine.  
DR PIR; A01886; K2HUF.  
DR HSSP; Q99M37; 1191.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON_TER 113  
  
SQ SEQUENCE 219 AA; 23944 MW; 7E1B92A14EAF8445 CRC64;  
  
Query Match 65.4%; Score 450; DB 2; Length 219;  
Best Local Similarity 75.2%; Pred. No. 5.1e-36;  
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;  
  
QY 20 DVNMTQPLTSLVITGQPASISCKSSQSLLYSNKTYLNWLLQRPQSPKRLIYLVSKLD 79  
Db 1 ELVMTQSPLSVSLGDAQSISCRSSQSLVHTNGNTYLNWLLQRPQSPKRLIYLVSKLD 79  
QY 80 SGVPDRFTGSGSDTFTLKISRVEAEDLGVCYVCGVTHPHTFGGTTKLEIKR 132  
Db 61 SGVPDRFTGSGSDTFTLKISRVEAEDLGVCYVCGVTHPHTFGGTTKLEIKR 113  
  
RESULT 10  
KV2E HUMAN  
ID KV2E HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain  
diversity."  
RL Nature 309:73-76(1984).  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; Z00009; -; NOT ANNOTATED_CDS.  
DR PIR; A01889; K2HUGM.  
DR HSSP; Q99M37; 1191.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT NON_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 117  
FT DOMAIN 5 27  
FT DOMAIN 28 43  
FT DOMAIN 44 58  
FT DOMAIN 59 65  
FT DOMAIN 66 97  
FT DOMAIN 98 106  
FT DOMAIN 107 116  
FT DISULFID 27 97  
FT NON_TER 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;  
  
Query Match 64.5%; Score 444; DB 1; Length 117;  
Best Local Similarity 73.3%; Pred. No. 9.8e-36;  
Matches 85; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
```



```

RL Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSP; B91639; K2HUCM.
DR PIR; P01751; INOB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 24 95
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 61.3%; Score 421.5; DB 1; Length 115;
Best Local Similarity 72.8%; Pred. No. 1.6e-33;
Matches 83; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 20 DVVMTQTPLTSLVITGPASISCKSSQSLLYS-NKTYLNWLLQRPQSPKRLIYLVSKL 78
Db 2 DIVMTQTPLSLPVTGPESASISCRSSQSLDSGDGNTYLNWYKAGSQPLLIIYLSYR 61
Qy 79 DSGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGTHTFPGGTGKLEIKR 132
Db 62 ASGVDRFSGSGDFTLKISRVAEDVGVIYCMQRLEIPYTFGGTKLEIRR 115

RESULT 14
KV2F MOUSE
ID KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM57S.
DR HSP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93

Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSP; B91639; K2HUCM.
DR PIR; P01751; INOB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 24 95
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 61.3%; Score 421.5; DB 1; Length 115;
Best Local Similarity 72.8%; Pred. No. 1.6e-33;
Matches 83; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 20 DVVMTQTPLTSLVITGPASISCKSSQSLLYS-NKTYLNWLLQRPQSPKRLIYLVSKL 78
Db 2 DIVMTQTPLSLPVTGPESASISCRSSQSLDSGDGNTYLNWYKAGSQPLLIIYLSYR 61
Qy 79 DSGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGTHTFPGGTGKLEIKR 132
Db 62 ASGVDRFSGSGDFTLKISRVAEDVGVIYCMQRLEIPYTFGGTKLEIRR 115

RESULT 14
KV2F MOUSE
ID KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVM57S.
DR HSP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93

FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 60.6%; Score 417; DB 1; Length 113;
Best Local Similarity 70.8%; Pred. No. 4.2e-33;
Matches 80; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 20 DVVMTQTPLTSLVITGPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DIVMTQTAPSAVTPGSEVSISCRSSKSLLSNGNTLYWFLQRPQSPQLLIYRMSNLA 60
Qy 80 SGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGTHTFPGGTGKLEIKR 132
Db 61 SGVDRFSGSGSGTAFTLRISRVAEDVGVIYCMQRLEIPYTFGGTKLEIKR 113

RESULT 15
Q6LEM8
ID Q6LEM8 PRELIMINARY; PRT; 112 AA.
AC Q6LEM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9;
RA Hifumi E., Mitsuda Y., Ohara K., Uda T.;
RT "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic
RT antibody light chain."
RL J. Immunol. Methods 269:283-298(2002).
DR EMBL; D85104; BAD00151.1; -.
DR HSSP; P01820; 1A70.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12443 MW; BAD3E14B90BCF122 CRC64;

Query Match 59.9%; Score 412; DB 2; Length 112;
Best Local Similarity 70.5%; Pred. No. 1.3e-32;
Matches 79; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 20 DVVMTQTPLTSLVITGPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DIVMTQTAPSVTPGSEVFTSCRSKSLLSNGNTLYWFLQRPQSPQLLIYRLEFLA 60
Qy 80 SGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGTHTFPGGTGKLEIK 131
Db 61 SGVDRFSGSGSGTAFTLRISRVAEDVGVIYCMQRLEIPYTFGGTKLEIK 112

Search completed: May 25, 2005, 15:56:05
Job time : 65.3423 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 65.427 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773A-13
Perfect score: 756
Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NFPYSYMDYWGQTSVTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	100.0	139	6	ABG74245 Mouse ant
2	678.5	89.7	138	8	ADI26639 Mouse ant
3	613	81.1	469	2	AAR40384 Monoclonal
4	602	79.6	138	3	AAV56873 MAB CT-M-
5	600	79.4	139	2	AAR29750 Anti-HMPG
6	597	79.0	139	2	AAR33950 CTMO1 VH.
7	593.5	78.5	140	2	AAW06213 MAB Co-1
8	593.5	78.5	140	2	AAW85061 Mouse Co-
9	593.5	78.5	140	6	ABU58895 Mouse ant
10	587.5	77.7	140	2	AAR09425 Co-1 Heav
11	587.5	77.7	148	8	ADM79825 Mouse IgG
12	587.5	77.7	253	8	ADM79829 D77 diabo
13	585	77.4	116	2	AAR79241 Heavy cha
14	577	76.3	135	2	AAW60866 Variable
15	577	76.3	135	3	AAV80293 Igm chime
16	577	76.3	590	2	AAW31751 H chain s
17	577	76.3	590	2	AAW71888 Anti-huma
18	577	76.3	590	3	AAAB12308 Anti-huma
19	574.5	76.0	140	2	AAR55554 DREG-200
20	569	75.3	135	2	AAW68548 Anti-CD33
21	569	75.3	135	4	AAW69682 Murine M1
22	569	75.3	135	8	ADO47773 Mouse M19
23	565.5	74.8	138	2	AAW50218 Amino aci
24	563.5	74.5	136	3	AAAB23815 Plasmid p
25	563.5	74.5	136	4	AAAG67491 Amino aci

26	563.5	74.5	136	5	AAW47629 Murine MA
27	563.5	74.5	136	5	ABG97806 Mouse MAB
28	563.5	74.5	136	5	ABG35309 Thrombopo
29	561.5	74.3	136	3	AAAB23813 Plasmid p
30	561.5	74.3	136	4	AAAG67489 Amino aci
31	561.5	74.3	136	5	AAW47627 Murine MA
32	561.5	74.3	136	5	ABG97804 Mouse MAB
33	561.5	74.3	136	5	ABG35307 Thrombopo
34	561.5	74.3	138	4	AAAB69688 Murine CM
35	561.5	74.3	138	8	ADO47789 Mouse CM
36	559	73.9	137	2	AAR05090 Heavy cha
37	559	73.9	137	3	AAV99845 Mouse par
38	559	73.9	139	2	AAR29009 p64-h2 pr
39	559	73.9	139	2	AAAS3328 KM-796 he
40	559	73.9	139	2	AAV28356 Antibody
41	559	73.9	139	2	AAV28384 Anti-GM2
42	558	73.8	118	3	AAAB11391 Murine II
43	557	73.7	137	2	AAW62445 81C6 heav
44	555.5	73.5	140	2	AAW21843 Heavy cha
45	555	73.4	561	2	AAV17415 Mouse imm

ALIGNMENTS

RESULT 1
ABG74245
ID ABG74245 standard; protein; 139 AA.

XX AC ABG74245;

XX XX 22-APR-2003 (first entry)

XX DE Mouse antibody 4D4 heavy chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;
immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
3E11; prostate-specific membrane antigen; zeta signalling chain;
CDalpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
small cell lung cancer; heavy chain variable region; mouse.

XX OS Mus sp.

XX PN US2002132983-A1.

XX XX 19-SEP-2002.

XX PD 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PR 30-NOV-2000; 2000US-0250089P.

XX PA (JUNG/) JUNGHANS R P.

XX XX Junghans RP;

XX PI WPI; 2003-208946/20.

XX DR N-PSDB; ABX16571.

XX XX New chimeric molecule useful in treating patients with disorders, such as
melanoma, neuroendocrine disorders, prostate and small cell lung cancer
comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 14-15; 35pp; English.

XX CC The invention relates to a chimaeric molecule comprising the GD3
(ganglioside antigen) binding domain of antibody MB3.6, with any of 3
variable gene sequences, or the PSMA (prostate-specific membrane antigen)
binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
sequences, the zeta signalling chain of the T cell receptor and an
intervening CD8alpha hinge in which cysteine residues have been mutated.
XX CC The chimeric molecules expressed in T cells or NK cells or other
effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 4D4 heavy chain variable region
 XX
 SQ Sequence 139 AA;

Query Match 100.0%; Score 756; DB 6; Length 139;
 Best Local Similarity 100.0%; Pred. No. 4.9e-58;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 DB 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 QY 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYWQLSSLTSENSAVYFCARGGN 120
 DB 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYWQLSSLTSENSAVYFCARGGN 120
 QY 121 FPSYAMDYWGQGSTVTSS 139
 DB 121 FPSYAMDYWGQGSTVTSS 139

RESULT 2
 ADI26639
 ID ADI26639 standard; protein; 138 AA.

AC ADI26639;
 DT 15-APR-2004 (first entry)
 DE Mouse anti-IgM antibody O1/A1/A4 JH protein.
 XX
 KW Mouse; antibody; IgM; remyelination; neuronal growth; autoantibody;
 KW demyelination disease; multiple sclerosis; central nervous system; CNS;
 KW axon; glial cell proliferation;
 KW Theiler's murine encephalomyelitis virus infection; CNS injury;
 KW spinal cord injury.
 XX
 OS Mus sp.

PN US2003185827-A1.
 XX
 PD 02-OCT-2003..
 XX
 PF 13-NOV-2001; 2001US-00010729.
 XX
 PR 29-APR-1994; 94US-00236520.
 PR 08-AUG-1996; 96US-00692084.
 PR 07-JAN-1997; 97US-00779784.
 PR 28-MAY-1999; 99US-00322862.
 PR 30-MAY-2000; 2000US-00580787.
 PR 05-DEC-2000; 2000US-00730473.
 XX

PA (MAYO-) MAYO FOUND.
 XX
 XX Rodriguez M, Miller DJ, Pease LR;
 XX
 DR WPI; 2004-119219/12.
 XX
 XX New human immunoglobulin M antibody for treating or preventing a
 PT demyelinating disease of the central nervous system in a human or
 PT domestic animal, such as multiple sclerosis.
 XX
 XX Example 4; Fig 12; 159pp; English.

XX The invention relates to an antibody (I) produced by injecting an
 CC immunocompetent host with an antibody peptide, and harvesting the
 CC antibody, where the peptide comprises a human anti-IgM antibody fragment

CC given in the specification, or active fragments. Also included are
 CC stimulating remyelination of central nervous system (CNS) axons in a
 CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial
 CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of mAb SH1GM22, SH1GM46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-IgM antibody (or
 CC fragment).
 XX
 SQ Sequence 138 AA;

Query Match 89.7%; Score 678.5; DB 8; Length 138;
 Best Local Similarity 92.1%; Pred. No. 2.7e-51;
 Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 DB 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 QY 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYWQLSSLTSENSAVYFCARGGN 120
 DB 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYWQLSSLTSENSAVYFCARGGN 120
 QY 121 FPSYAMDYWGQGSTVTSS 139
 DB 121 FYWY-FDVWAGTGTVTSS 138

RESULT 3
 AAR40384
 ID AAR40384 standard; protein; 469 AA.
 XX
 AC AAR40384;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 08-FEB-1994 (first entry)
 XX
 DE Monoclonal antibody M(alpha)2-3 Heavy-chain.

XX anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin;
 KW bispecific bivalent antibody; cell-targeting; cytotoxic agent.
 XX

Unidentified.

OS
XX Key Location/Qualifiers
FH Peptide 1..19
FT Region /label= signal_peptide
FT Region 20..139
FT FT /label= variable
FT Region 140..236
FT FT /label= constant
FT Region 237..252
FT FT /label= joining
FT Region 253..362
FT FT /label= constant
FT Region 363..469
FT FT /label= constant

EP556111-A1.

PN XX

PD 18-AUG-1993.

XX 09-FEB-1993; 93EP-00400323.

PF 11-FEB-1992; 92FR-00001505.

PR 11-FEB-1992; 92FR-00001505.

XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PA Boulain J, Ducancel F, Gillet D, Menez A;

PI WPI; 1993-260351/33.

XX N-PSDB; AAQ48037.

DR New immunoglobulin hybrid proteins - with immunoglobulin fragments linked

XX to dimeric protein, for diagnostic or therapeutic use.

PT Example 1; Fig 3A; 37pp; French.

XX A fragment of the heavy chain (VH + CH1) from the anti-snake small

CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from

CC hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain

CC fragment (VL + CL) was amplified from the same source using primers

CC AAQ48041 and AAQ48042. The two amplified fragments were inserted into the

CC same vector; the H-chain fragment was inserted (in-frame) between codons

CC 6-7 of the phoA coding sequence and the L-chain fragment was inserted

CC into a cassette which contained a phoA S-D sequence, a signal peptide and

CC the first 6 codons of phoA. The cassette was positioned between the

CC termination codon and the transcription termination sequence of phoA. The

CC fusion construct is expected to encode a hybrid protein comprising two

CC identical Ab-derived units. The invention also covers hybrid proteins

CC containing two different Ab-derived units (i.e. to produce bispecific

CC antibodies). When a toxic protein is used in place of phoA, the hybrid

CC molecules can be used as cell-targeting therapeutic agents. (Updated on

CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct

CC PN field.)

XX Sequence 469 AA;

SQ Query Match 81.1%; Score 613; DB 2; Length 469;

XX Best Local Similarity 80.6%; Pred. No. 5e-45;

XX Matches 112; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

XX 1 MGWRWIFLLSGTAGVHCQVQLQSGPGLVPGASVKISCKASGYTFTDYYINWKQKP 60

XX 1 MGWSWIFLLSGTAGVHCQVQLQSGPGLVPGASVKISCKASGYTFTDYYINWKQKP 60

XX 61 GQGLEWIGWIPGDSGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

XX 61 GQGLEWIGWIPASGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

XX 121 FPSYAMDYWGQGTSTVTVSS 139

XX 121 ATATLLDYWGQGTSTVTVSS 139

RESULT 4

AA56873

ID AAY56873 standard; protein; 138 AA.

XX AC AAY56873;

XX DT 14-APR-2000 (first entry)

XX DE MAb CT-M-01 heavy chain VH domain.

XX KW Cytotoxic; drug conjugate; humanized; monoclonal antibody; CT-M-01;

XX KW human milk fat globule; growth inhibition.

XX OS Homo sapiens.

XX PN US6015562-A.

XX PD 18-JAN-2000.

XX PF 16-FEB-1996; 96US-00603024.

XX PR 22-SEP-1992; 92US-00948277.

XX PR 06-OCT-1993; 93US-00132725.

XX PR 31-OCT-1994; 94US-00332025.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Hamann PR, Hinman LM;

XX DR WPI; 2000-126309/11.

XX DR N-PSDB; AAZ46912.

XX PT New cytotoxic drug conjugates are useful for inhibiting the growth of

XX PT unwanted cells.

XX PS Disclosure; Col 21-22; 37pp; English.

XX CC The invention relates to cytotoxic drug conjugates of a specified

CC formula. The conjugate comprise a humanized monoclonal antibody (Mab)

CC hu-CT-M-01 reactive to human milk fat globule, its antigen-recognizing

CC fragments, or chemically manipulated counterparts. The cytotoxic drug

CC conjugates are useful for inhibiting the growth of unwanted cells. The

CC present sequence represents the Mab CT-M-01 heavy chain VH domain

XX Sequence 138 AA;

SQ Query Match 79.6%; Score 602; DB 3; Length 138;

XX Best Local Similarity 81.2%; Pred. No. 1.2e-44;

XX Matches 112; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

XX QY 1 MGWRWIFLLSGTAGVHCQVQLQSGPGLVPGASVKISCKASGYTFTDYYINWKQKP 60

XX Db 1 MENSWVFLFLSVTTGVHCQVQLQSGPGLVPGASVKISCKASGYTFTDYYINWKQKP 60

XX QY 61 GQGLEWIGWIPGDSGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

XX Db 61 GQGLEWIGWIDPGSGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAREKT 120

XX QY 121 FPSYAMDYWGQGTSTVTVSS 138

XX Db 121 TYYAMDYWGQGTSTVTVSS 138

XX RESULT 5

AAW29750

ID AAW29750 standard; protein; 139 AA.

XX AC AAW29750;

XX DT 25-MAR-2003 (revised)

XX DT 14-JAN-1998 (first entry)

XX DE Anti-HMFG Mab CTM01 heavy chain variable region.

XX Humanised antibody; CDR-grafted antibody; chimeric antibody; CTM01;
 KW complementarity determining region; human milk fat globule; HMFG;
 KW monoclonal antibody; MAb; mouse; cancer; breast cancer; ovary carcinoma;
 KW lung cancer; uterus cancer; diagnosis; therapy.
 XX Mus musculus.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Leader_peptide
 FT Misc-difference 344
 FT /note= "encoded by ACG"
 XX
 XX EP781845-A2.
 XX
 XX
 XX 02-JUL-1997.
 XX
 XX 24-SEP-1992; 97EP-00200482.
 XX
 XX 26-SEP-1991; 91GB-00020467.
 PR
 PR 24-SEP-1992; 92EP-00308680.
 XX
 XX (CLLT) CELLTECH THERAPEUTICS LTD.
 PA
 XX Hamann PR, Adair JR, Owens RJ, Baker TS, Lyons AH, Hinman LM;
 PI Menendez AT;
 XX
 XX WPI; 1997-334902/31.
 DR N-PSDB; AAT85854.
 XX
 XX DNA encoding composite heavy and light chains of humanised antibody -
 PT specific for human milk fat globule, useful in cancer diagnosis or
 PT therapy.
 XX
 PS Claim 1; Page 17-18; 53pp; English.
 XX
 XX This polypeptide sequence comprises the heavy chain variable region VH of
 CC murine anti-human milk fat globule (HMFG) monoclonal antibody CTM01. The
 CC sequence was deduced from an isolated cDNA clone (see AAT85854). CTM01
 CC recognises a polymorphic epithelial mucin of HMFG. The CTM01 VH region
 CC can be used in the design of chimeric humanised antibodies or CDR-grafted
 CC humanised anti-HMFG antibodies. Preferred humanised antibody heavy chains
 CC include residues 2, 26-35, 37, 50-65, 71, 73, 95-105 and 107 (Kabab
 CC numbering) of murine CTM01 VH, and may also include residues 6, 23, 49,
 CC 76, 78, 80, 88 and 91, in a human LAY POM, TUR, TEI, KOL, NEWN, REI or EU
 CC framework. The recombinant VH can be expressed in transformed host cells.
 CC Humanised antibodies may be conjugated with labels or drugs (especially
 CC methylthio antitumour agents) and used for diagnosis or therapy of
 CC human carcinomas, e.g. of the ovary, breast, uterus and lung. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
 CC field.)
 XX
 XX Sequence 139 AA;
 SQ
 Query Match 79.4%; Score 600; DB 2; Length 139;
 Best Local Similarity 80.8%; Pred. No. 1.8e-44;
 Matches 112; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MGRWRIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 Db 1 MEWSWVFLFSLVTTGVHCQIQQLQQSGPELVKPGASVKISCKASGYTFTDYINWVKQRP 60
 QY 61 GQGLEWIGWYIPDGGTNYNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
 Db 61 GQGLEWIGWIDPGSGNTKYNEKFGKATLTVDTSSTAYMQLSSLTSEDVAVYFCAREKI 120
 QY 121 FPSYANDYWGQGSTVTSS 139
 Db 121 TTYIANDYWGQGSTVTSA 139

RESULT 6

AAR33950
 ID AAR33950 standard; protein; 139 AA.
 XX
 AC AAR33950;
 XX 25-MAR-2003 (revised)
 DT 16-JUL-1993 (first entry)
 XX
 XX CTM01 VH.
 XX Heavy; light; chain; variable; domain; CTM01; PCR; primer; carcinoma;
 KW immunoglobulin; murine; monoclonal; antibody; MAb; IGG-kappa; ovary;
 KW humanised; diagnosis; therapy; breast; uterus; lung.
 XX
 XX Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Signal peptide"
 FT Protein 20..139
 FT /note= "Mature protein"
 XX
 XX EP534742-A1.
 XX
 XX 31-MAR-1993.
 XX
 XX 24-SEP-1992; 92EP-00308680.
 XX
 XX 26-SEP-1991; 91GB-00020467.
 XX
 XX (CLLT) CELLTECH LTD.
 PA
 PA (CLLT) CELLTECH THERAPEUTICS LTD.
 XX
 XX Adair JR, Hamann PR, Owens RJ, Baker TS, Lyons AH, Hinman LM;
 PI Menendez AT;
 XX
 XX WPI; 1993-102837/13.
 DR N-PSDB; AAQ38877.
 XX
 XX Anti-human milk fat globule humanised antibodies - useful as conjugate
 PT for in-vivo diagnosis and therapy of e.g. ovarian or breast cancer.
 XX
 XX Disclosure; Page 17-18; 57pp; English.
 XX
 XX The sequences given in AAR33950-51 represent the heavy and light chain
 CC variable domains of CTM01 respectively. The DNA encoding these peptides
 CC was isolated by PCR using the primer sequences given in AAQ38879-80.
 CC Examination of these amino acid sequences revealed considerable homology
 CC with other characterised immunoglobulin genes. The murine monoclonal
 CC antibody (MAb), CTM01, was confirmed to be an IGG-kappa antibody. CTM01
 CC was used in the production of a humanised antibody for in vivo diagnosis
 CC and therapy of carcinomas of ovary, breast, uterus and lung. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 XX Sequence 139 AA;
 SQ
 Query Match 79.0%; Score 597; DB 2; Length 139;
 Best Local Similarity 79.9%; Pred. No. 3.4e-44;
 Matches 111; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MGRWRIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 Db 1 MEWSWVFLFSLVTTGVHCQIQQLQQSGPELVKPGASVKISCKASGYTFTDYINWVKQRP 60
 QY 61 GQGLEWIGWYIPDGGTNYNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
 Db 61 GQGLEWIGWIDFGSGNTKYNEKFGKATLTVDTSSTAYMQLSSLTSEDVAVYFCAREKT 120
 QY 121 FPSYANDYWGQGSTVTSS 139
 Db 121 TTYIANDYWGQGSTVTSA 139

RESULT 7

AAW06213
 ID AAW06213 standard; protein; 140 AA.
 XX AC AAW06213;
 XX DT 25-MAR-2003 (revised)
 DT 13-FEB-1997 (first entry)
 XX DE MAb Co-1 heavy chain variable region.
 XX KW Chimeric antibody; monoclonal antibody; Co-1; antibody engineering;
 KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
 KW ovary carcinoma; cancer; diagnosis; therapy; heavy chain.
 XX OS Mus sp.
 XX PN US5576184-A.
 XX PD 19-NOV-1996.
 XX PF 27-DEC-1994; 94US-00364001.
 XX PR 06-SEP-1988; 88US-00240624.
 PR 08-SEP-1988; 88US-00241744.
 PR 13-SEP-1988; 88US-00243739.
 PR 04-OCT-1988; 88US-00253002.
 PR 19-JUN-1989; 89US-00367641.
 PR 21-JUL-1989; 89US-00382768.
 PR 06-MAY-1991; 91US-00659401.
 XX PA (XOMA) XOMA CORP.
 XX PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
 XX WPI; 1997-011249/01.
 XX DR N-PSDB; AAT43438.
 XX PT Chimeric mouse-human antibodies - recognise a human tumour antigen, used
 PT for the treatment and diagnosis of human cancers.
 XX PS Example 3; Fig 22; 102pp; English.

XX CC The heavy chain variable region (AAW06213) of mouse monoclonal antibody
 CC Co-1 is the product of a cDNA clone (AAT43438) isolated from a Co-1
 CC hybridoma cDNA library. MAb Co-1 (IgG1) binds to an antigen that is
 CC expressed on the surface of human lung, breast, colon and ovary
 CC carcinomas, but not on most normal adult tissues. The heavy chain and
 CC light chain variable regions (see also AAW06214) of Co-1 can be linked to
 CC human constant regions and expressed in transformed host cells. Novel
 CC mouse-human chimeric antibodies (see also AAW06209-12 and AAW06215-18)
 CC can be produced that have specificity to human tumour antigens and can be
 CC used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX SQ Sequence 140 AA;

Query Match 78.5%; Score 593.5; DB 2; Length 140;
 Best Local Similarity 81.4%; Pred. No. 6.8e-44;
 Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
 Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSYDINWVKQRP 60
 Db 1 MEWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKMSCKASGYTTSYVMHWVKQRP 60
 Qy 61 GQGLEWICWIPYDGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120
 Db 61 GQGLEWICWIPYDGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120
 Qy 121 FDSYMDYWGQGTSTVTVSS 139
 Db 121 FDSYMDYWGQGTSTVTVSS 140

RESULT 8

AAW85061
 ID AAW85061 standard; protein; 140 AA.
 XX AC AAW85061;
 XX DT 20-MAR-2003 (revised)
 DT 16-APR-1999 (first entry)
 XX DE Mouse Co-1 heavy chain variable region.
 XX KW Heavy chain variable region; murine antibody Co-1; antibody ING-1;
 KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
 KW treatment; human cancer.
 XX OS Mus sp.
 XX PN US5843685-A.
 XX PD 01-DEC-1998.
 XX PF 06-JUN-1995; 95US-00466034.
 XX PR 06-SEP-1988; 88US-00240624.
 PR 08-SEP-1988; 88US-00241744.
 PR 13-SEP-1988; 88US-00243739.
 PR 04-OCT-1988; 88US-00253002.
 PR 19-JUN-1989; 89US-00367641.
 PR 21-JUL-1989; 89US-00382768.
 PR 06-SEP-1989; 89WO-US003852.
 PR 06-MAY-1991; 91US-00659401.
 PR 27-DEC-1994; 94US-00364001.
 XX PA (XOMA) XOMA CORP.
 XX PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;
 XX WPI; 1999-044574/04.
 XX DR N-PSDB; AAW71157.
 XX PT Chimeric antibody specific for human tumour antigen - useful as
 PT immunoassay, imaging or antitumour agent.
 XX PS Example 3; Fig 22; 92pp; English.

XX CC The present sequence represents the heavy chain variable region of murine
 CC antibody Co-1. The sequence was used to create chimeric mouse-human
 CC immunoglobulins which recognise the human tumour antigen bound by
 CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
 CC chimeric antibodies also have an antigen-binding site that competitively
 CC inhibits the binding of antibody ING-1, and mediate complement-dependent
 CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to
 CC target cells. The chimeric antibodies can be used for therapeutic
 CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
 CC correct PR field.)
 XX SQ Sequence 140 AA;

Query Match 78.5%; Score 593.5; DB 2; Length 140;
 Best Local Similarity 81.4%; Pred. No. 6.8e-44;
 Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
 Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSYDINWVKQRP 60
 Db 1 MEWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKMSCKASGYTTSYVMHWVKQRP 60
 Qy 61 GQGLEWICWIPYDGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120
 Db 61 GQGLEWICWIPYDGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120
 Qy 121 FDSYMDYWGQGTSTVTVSS 139
 Db 121 FDSYMDYWGQGTSTVTVSS 140

121 FDYSYVMDYWGQGTSTVSS 140

| | | | | | | | | | | | | |

121 FDYSYVMDYWGQGTSTVSS 140

RESULT 9
ABU58895
ID ABU58895 standard; protein; 140 AA.

XX ABU58895;

DT 16-APR-2003 (first entry)

XX Mouse antibody heavy chain variable region #3.

XX Mouse; human tumour antigen; anti-human tumour antigen-antibody;

KW ING-1 antibody; cell line H9812; immunoassay; imaging; tumour diagnosis;

KW tumour therapy; cytostatic; heavy chain variable region.

XX

OS Mus sp.

XX US6461824-B1.

PN 08-OCT-2002.

PD

XX 06-JUN-1995; 95US-00467142.

XX 06-SEP-1988; 88US-00240624.

PR 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

PR 06-SEP-1989; 89WO-US003852.

PR 06-MAY-1991; 91US-00659401.

PR 27-DEC-1994; 94US-00364001.

XX (XOMA) XOMA TECHNOLOGY LTD.

XX

PA Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX

PI WPI; 2003-196707/19.

XX DR N-PSDB; ABK79237.

XX

XX Antibody for detecting antigen in animal or killing cells carrying

PT antigen comprises human constant region and variable region having

PT specificity for human tumor antigen bound by ING-1 antibody.

XX

XX Example 3; Fig 22; 101pp; English.

XX

XX The invention describes an antibody comprising a human constant region

CC and a variable region having specificity for the human tumour antigen

CC bound by the ING-1 antibody, where the ING-1 is produced by cell line

CC HB9812 as deposited with ATCC, and the antibody has the same affinity as

CC the ING-1 for the human tumour antigen. The antibody is useful in an

CC immunoassay method for detecting an antigen in a sample by contacting a

CC label-detectable antigen in the sample with the antibody, detecting the

CC label and relating the detected label to the presence of the antigen; for

CC use in an imaging method for revealing the presence of a label-detectable

CC antigen in an animal by contacting the antibody with a part of the animal

CC suspected of containing the antigen, detecting the label and relating the

CC detected label to the presence of the antigen; and for killing cells

CC carrying an antigen by contacting the cells with the antibody and

CC allowing the killing to occur. The antibodies are useful in tumour

CC diagnosis and therapy. The chimeric antibodies bind to the surface of

CC human tumour cells but do not bind detectably to normal cells, e.g.,

CC fibroblasts, endothelial cells or epithelial cells in the major organs.

CC The high biological activity of the chimeric antibodies against human

CC tumour cell lines combined with minimal reactivity with normal tissues

CC imply that these antibodies may mediate selective destruction of

CC malignant tissue. The presence of human rather than murine antigenic

CC determinants on the chimeric antibodies increases their resistance to

CC rapid clearance from the body relative to the original murine mAbs. This

CC resistance to clearance enhances the potential utility of these chimeric

CC

CC antibodies, as well as their derivatives, in tumour diagnosis and
CC therapy. This is the amino acid sequence of a mouse antibody heavy chain
CC variable region used in the creation of an anti-human tumour antigen-
CC antibody

XX Sequence 140 AA;

Query Match 78.5%; Score 593.5; DB 6; Length 140;

Best Local Similarity 81.4%; Pred. No. 6.8e-44;

Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGRWIFLLSGLTAGVHCQVQLQSGPELVKPGALVKISKCKASGYTFTSYDINWVKQRP 60

Db 1 MEWSMIFLLSGLTAGVHSEVQLQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQRP 60

QY 61 GQGLEWIGWYFGDGTNNEKFKGKATLTADKSSSTAYMQLSSLTSENNAVYFCARGN 120

Db 61 GQGLEWIGWYFGDGTNNEKFKGKATLTADKSSSTAYMQLSSLTSENNAVYFCARGN 120

QY 121 PP-SYAMDYWGQGTSTVTVSS 139

Db 121 FDYSYVMDYWGQGTSTVTVSS 140

RESULT 10

AAR09425

ID AAR09425 standard; protein; 140 AA.

XX

AC AAR09425;

XX 25-MAR-2003 (revised)

DT 04-MAR-1993 (first entry)

XX

DE Co-1 Heavy Chain V Region (mouse).

XX

KW Monoclonal antibody; chimera; light; heavy; chain; constant; variable;

KW antigen; diagnosis; cancer; tumour.

XX

OS Mus musculus.

XX

PN WO9002569-A.

XX

XX 22-MAR-1990.

XX

PF 08-SEP-1988; 88US-00241744.

XX

PR 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

XX

XX (ITGE-) INT GENETIC ENG INC.

PA (INGE-) INGENE INT GENETIC.

XX

PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX

XX WPI; 1990-115825/15.

DR N-PSDB; AAQ08607.

XX

XX Chimeric mouse-human antibodies - prep. using genes coding for constant

PT human region murine variable region, esp. to 3 tumour antigen.

XX

PS Claim 13; Page 123 + Fig 22; 173pp; English.

XX

XX The sequence is used in the prodn. of a chimeric antibody mol. comprising

CC two light chains and two heavy chains, each having a constant region

CC (human) and a variable region (murine) having specificity to an antigen

CC bound by murine monoclonal antibody (MAB) Co-1. The chimeric antibodies

CC can be used for any purpose for which the original murine MABs can be

CC used, with the advantage that they are more compatible with the human

CC body. They are esp. used for the diagnosis and treatment of cancer.

CC

CC (Updated on 25-MAR-2003 to correct PA field.)

CC

XX Sequence 140 AA;
SQ Query Match 77.7%; Score 587.5; DB 2; Length 140;
Best Local Similarity 80.7%; Pred. No. 2.3e-43;
Matches 113; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Qy 1 MGNWIFLLSSTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60
Db 1 MGNWIFLLSSTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60
Qy 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120
Db 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120
Qy 121 FSYVMDYWGQGTSTVTVSS 139
Db 121 FSYVMDYWGQGTSTVTVSS 140

RESULT 11
ADM79825
ID ADM79825 standard; protein; 148 AA.
XX AC ADM79825;
XX 15-JUL-2004 (first entry)
XX Mouse IgG2b heavy chain protein SEQ ID NO:2.
XX cell death-inducing agent; human leukocyte antigen; HLA; antibody;
KW 2D7 antibody; 2D7 antibody degradation product;
KW cell proliferation inhibition; antitumour; autoimmune disease;
KW cytostatic; immunosuppressive; antiinflammatory; dermatological; cancer;
KW Crohn's disease; systemic lupus erythematosus; mouse; IgG2b heavy chain.
XX Mus musculus.
OS
XX WO2004033499-A1.
XX 22-APR-2004.
XX 10-OCT-2003; 2003WO-JP013063.
XX 11-OCT-2002; 2002JP-00299289.
XX (CHUS) CHUGAI SEIYAKU KK.
XX (OZAK/) OZAKI S.
XX (ABEM/) ABE M.
XX Ozaki S, Abe M, Teuchiya M, Kimura N, Kawai S;
XX WPI; 2004-330447/30.
XX N-PSDB; ADM79824.
XX Cell death-inducing agents containing degradation product of antibody particularly diabody recognizing human leukocyte antigen (HLA), applicable in antitumor agents and remedies for autoimmune diseases for treating e.g. cancer.
XX Claim 6; SEQ ID NO 2; 106pp; Japanese.
XX The present invention describes cell death-inducing agents containing the degradation product of an antibody which can recognise human leukocyte antigen (HLA). Also described: (1) a degradation product of the 2D7 antibody; (2) a similar degradation product of an antibody which is: (a) one containing an amino acid sequence of (SEQ ID NO:6) with 253 amino acids; (b) one based on the sequence of (SEQ ID NO:6) but with some amino acids substituted, deleted, inserted and/or added and being functionally equivalent to the parent; (c) one containing the CDR amino-acid sequences of (SEQ ID NO:2) and (SEQ ID NO:4) with 148 and 144 amino acids respectively; or (d) one based on the sequence of (SEQ ID NO:2) and (SEQ ID NO:4) but with some amino acids substituted, deleted, inserted and/or

CC added and being functionally equivalent to the parent; (3) a process for producing an antibody with an increase of activity by degrading a HLA-recognising antibody, or by degrading 2D7 antibody; (4) cell death-inducing agents containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody as active ingredient; (5) agents for inhibiting cell proliferation containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody; (6) antitumour agents containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody; and (7) remedies for autoimmune diseases containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has cytostatic, immunosuppressive, antiinflammatory and dermatological activities. The cell death-inducing agents are applicable in antitumour agents and remedies for autoimmune diseases for treating e.g. cancer, Crohn's disease and systemic lupus erythematosus. The present sequence represents a mouse IgG2b heavy chain, which is used in the exemplification of the present invention.
XX Sequence 148 AA;
SQ Query Match 77.7%; Score 587.5; DB 8; Length 148;
Best Local Similarity 79.1%; Pred. No. 2.4e-43;
Matches 110; Conservative 11; Mismatches 13; Indels 5; Gaps 1;

Qy 1 MGNWIFLLSSTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60
Db 1 MGNWIFLLSSTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60
Qy 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120
Db 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120
Qy 121 FSYVMDYWGQGTSTVTVSS 139
Db 121 FSYVMDYWGQGTSTVTVSS 134

RESULT 12
ADM79829
ID ADM79829 standard; protein; 253 AA.
XX AC ADM79829;
XX 15-JUL-2004 (first entry)
XX 2D7 diabody (2D7DB) protein SEQ ID NO:6.
XX cell death-inducing agent; human leukocyte antigen; HLA; antibody;
KW 2D7 antibody; 2D7 antibody degradation product;
KW cell proliferation inhibition; antitumour; autoimmune disease;
KW cytostatic; immunosuppressive; antiinflammatory; dermatological; cancer;
KW Crohn's disease; systemic lupus erythematosus; 2D7 diabody; 2D7DB.
XX Synthetic.
XX WO2004033499-A1.
XX 22-APR-2004.
XX 10-OCT-2003; 2003WO-JP013063.
XX 11-OCT-2002; 2002JP-00299289.
XX (CHUS) CHUGAI SEIYAKU KK.
XX (OZAK/) OZAKI S.
XX (ABEM/) ABE M.
XX Ozaki S, Abe M, Teuchiya M, Kimura N, Kawai S;
XX WPI; 2004-330447/30.
XX N-PSDB; ADM79828.
XX Cell death-inducing agents containing degradation product of antibody

particularly diably recognizing human leukocyte antigen (HLA), applicable in antitumor agents and remedies for autoimmune diseases for treating e.g. cancer.

Claim 6; SEQ ID NO 6; 106pp; Japanese.

The present invention describes cell death-inducing agents containing the degradation product of an antibody which can recognise human leukocyte antigen (HLA). Also described: (1) a degradation product of the 2D7 antibody; (2) a similar degradation product of an antibody which is: (a) one containing an amino acid sequence of (SEQ ID NO:6) with 253 amino acids; (b) one based on the sequence of (SEQ ID NO:6) but with some amino acids substituted, deleted, inserted and/or added and being functionally equivalent to the parent; (c) one containing the CDR amino-acid sequences of (SEQ ID NO:2) and (SEQ ID NO:4) with 148 and 144 amino acids respectively; or (d) one based on the sequence of (SEQ ID NO:2) and (SEQ ID NO:4) but with some amino acids substituted, deleted, inserted and/or added and being functionally equivalent to the parent; (3) a process for producing an antibody with an increase of activity by degrading a HLA-recognising antibody, or by degrading 2D7 antibody; (4) cell death-inducing agents containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody as active ingredient; (5) agents for inhibiting cell proliferation containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody; (6) antitumor agents containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody; and (7) remedies for autoimmune diseases containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has cytostatic, immunosuppressive, antiinflammatory and dermatological activities. The cell death-inducing agents are applicable in antitumor agents and remedies for autoimmune diseases for treating e.g. cancer. Crohn's disease and systemic lupus erythematosus. The present sequence represents a 2D7 antibody (2D7DB), which is used in the exemplification of the present invention.

Sequence 253 AA;

Query Match 77.7%; Score 587.5; DB 8; Length 253;

Best Local Similarity 79.4%; Pred. No. 4.3e-43; Mismatches 11; Indels 5; Gaps 1;

Matches 110; Conservative 11; Mismatches 13; Indels 5; Gaps 1;

QY 1 MGRWIFLLSITAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 DB 1 MRWSIFLLSITAGVHCQVQLQSGPELVKPGASVMSCKASGYTFTDIFHWVKQRP 60
 QY 61 GQGLEWIGWYIPGDDGTYNEKPKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
 DB 61 GQGLEWIGWYIPGDDGTYNEKPKGKATLTADKSSSTAYMQLSSLTSENSAVYFCVRSD 120
 QY 121 FPSYANDYWGQTSVTSS 139
 DB 121 F-----DYWGQGTTLTVSS 134

RESULT 13

AAR79241
 ID AAR79241 standard; protein; 116 AA.

AC AAR79241;

DT 25-MAR-2003 (revised)

DT 21-DEC-1995 (first entry)

XX Heavy chain variable region for monoclonal antibody 4A10.

XX Monoclonal antibody; heavy metal; mercury; variable region; heavy chain.

XX Synthetic.

XX W09520607-A1.

XX 03-AUG-1995.

PF

27-JAN-1995; 95WO-US001199.

XX

PR 27-JAN-1994; 94US-00187407.

XX

PA (BION-) BIONEERASKA INC.

XX

PI Lopez O, Wylie DE, Wagner F;

XX

DR WPI: 1995-275415/36.

DR

XX N-PSDB; AAQ97498.

XX

PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from

PT

monoclonal antibodies, used for detecting, removing, adding or

PT

neutralising heavy metals.

XX

PS Claim 13; Page 54; 106pp; English.

XX

Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F6, 2D5, 5B6 and 3E8) were producing MAbs that were strongly positive against glutathione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand cDNA synthesis was catalyzed by MuLV reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5' end of the CH1 domain of the heavy chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the variable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplify the MAb 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings. The descriptions in the sequence listings are used here. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 116 AA;

Query Match 77.4%; Score 585; DB 2; Length 116;

Best Local Similarity 93.3%; Pred. No. 3.1e-43; Mismatches 3; Indels 4; Gaps 1;

Matches 112; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 20 QVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWYIPGDDGTYN 79

DB 1 EVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWYIPGDDGTYN 60

QY 80 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGNPFPSYANDYWGQTSVTSS 139

DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGNPFPSYANDYWGQTSVTSS 116

RESULT 14

AAW60866

ID AAW60866 standard; protein; 135 AA.

AC AAW60866;

XX 10-SEP-1998 (first entry)

DT Variable region of an anti-Fas antibody heavy chain.

XX Variable region; heavy chain; anti-Fas antibody; human; mouse;

XX immunoglobulin G; IgG; light chain; treatment; diagnosis;

XX autoimmune disease.

XX Mus sp.

XX JP10165178-A.


```

XX PD 23-JUN-1998.
XX PF 01-JUL-1997; 97JP-00191769.
XX PR 02-JUL-1996; 96JP-00172228.
XX PR 09-OCT-1996; 96JP-00268737.
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX DR WPI; 1998-406105/35.
XX DR N-PSDB; AAV37264.
XX PT DNA encoding, e.g. variable region of anti-Fas antibody - useful for,
XX e.g. diagnosis and treatment of auto-immune diseases.
XX PS Claim 7; Page 13; 16pp; Japanese.
XX CC The present sequence represents a variable region of the heavy chain of
XX an anti-Fas antibody. The constant region of the heavy chain is derived
XX from human immunoglobulin G (IgG). The anti-Fas antibody can be used for
XX the treatment and diagnosis of autoimmune diseases
XX SQ Sequence 135 AA;

Query Match 76.3%; Score 577; DB 2; Length 135;
Best Local Similarity 78.4%; Pred. No. 1.8e-42;
Matches 109; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKCKASYTFTSYDINWVKQRP 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKCKASYTFTDYNMHWKQSH 60

QY 61 GQGLEWIGWIYPGDTGTYNEKFKGKATLTADKSSSTAYMQLSSLTSNSAVYFCARGN 120
DB 61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMELRLSLTSDSAVYVCARS-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --YYAMDYWGQGTSTVTVSS 135

RESULT 15
AA80293
ID AAY80293 standard; protein; 135 AA.
AC AAY80293;
XX DT 30-MAY-2000 (first entry)
XX DE IgM chimeric antibody heavy chain variable region SEQ ID NO:1.
XX KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
XX KW diagnosis; CDR; complementarity determining region; apoptosis;
XX KW immunosuppressive.
XX OS Mus sp.
XX OS Synthetic.
XX PN JP2000014383-A.
XX PD 18-JAN-2000.
XX PF 03-JUL-1998; 98JP-00204318.
XX PR 03-JUL-1998; 98JP-00204318.
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX DR WPI; 2000-199626/18.
XX DR N-PSDB; AAZ95282.
XX PT Novel recombinant antibody used for treating and diagnosing autoimmune

```

```

PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX PS Example 1; Page 9-10; 25pp; Japanese.
XX CC The present invention describes a recombinant antibody (A) which binds to
XX fas antigen, and controls and induces apoptosis in cells which expressed
XX fas antigen. The complementarity determining regions (CDR) of (A) contain
XX amino acid sequences obtained from a mammal other than human, other
XX regions contain amino acid sequences from human and they partly contain
XX modified amino acids. (A) has immunosuppressive activity. (A) is used for
XX treating and/or diagnosing autoimmune diseases. The present sequence
XX represents an immunoglobulin M chimeric antibody heavy chain variable
XX region from an example from the present invention
XX SQ Sequence 135 AA;

Query Match 76.3%; Score 577; DB 3; Length 135;
Best Local Similarity 78.4%; Pred. No. 1.8e-42;
Matches 109; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKCKASYTFTSYDINWVKQRP 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKCKASYTFTDYNMHWKQSH 60

QY 61 GQGLEWIGWIYPGDTGTYNEKFKGKATLTADKSSSTAYMQLSSLTSNSAVYFCARGN 120
DB 61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMELRLSLTSDSAVYVCARS-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --YYAMDYWGQGTSTVTVSS 135

Search completed: May 25, 2005, 15:47:20
Job time : 67.427 secs

```

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 17.3265 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-13
Perfect score: 756
Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NPPSYAMDYWGQTSVTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	603	79.8	139	1	US-08-253-877C-8
2	603	79.8	139	2	US-08-452-164A-8
3	602	79.6	138	3	US-08-603-024-2
4	585	77.4	116	2	US-08-888-366-2
5	574.5	76.0	140	5	PCT-US93-11612-4
6	569	75.3	135	1	US-07-634-278-69
7	569	75.3	135	1	US-08-477-728-69
8	569	75.3	135	1	US-08-474-040-69
9	569	75.3	135	1	US-08-487-200-69
10	569	75.3	135	3	US-08-484-537-69
11	565.5	74.8	138	4	US-09-254-180C-143
12	565.5	74.8	140	3	US-08-579-378A-4
13	561.5	74.3	138	1	US-07-634-278-85
14	561.5	74.3	138	1	US-08-477-728-85
15	561.5	74.3	138	1	US-08-474-040-85
16	561.5	74.3	138	1	US-08-487-200-85
17	561.5	74.3	138	3	US-08-484-537-85
18	559	73.9	139	1	US-08-137-117D-35
19	559	73.9	139	2	US-08-436-717-35
20	559	73.9	139	2	US-08-116-778E-1
21	559	73.9	139	2	US-08-438-562-1
22	559	73.9	139	2	US-08-483-528B-91
23	557	73.7	137	1	US-08-392-419-2
24	556	73.5	151	3	US-08-513-968-34
25	555.5	73.5	140	3	US-08-836-561-27
26	555.5	73.5	140	4	US-09-434-122-27
27	555	73.4	561	3	US-09-192-545-2

28	552	73.0	137	2	US-08-116-778E-3	Sequence 3, Appli
29	552	73.0	137	2	US-08-438-562-3	Sequence 3, Appli
30	552	73.0	137	2	US-08-483-528B-93	Sequence 93, Appl
31	550	72.8	135	1	US-08-137-117D-27	Sequence 27, Appl
32	550	72.8	135	2	US-08-436-717-27	Sequence 27, Appl
33	548	72.5	137	4	US-08-647-468-153	Sequence 153, App
34	548	72.5	137	4	US-08-647-468-154	Sequence 154, App
35	537.5	71.1	138	1	US-08-458-516-7	Sequence 7, Appli
36	536.5	71.0	136	5	PCT-US93-11611-4	Sequence 4, Appli
37	536	70.9	135	1	US-07-634-278-19	Sequence 19, Appl
38	536	70.9	135	1	US-08-477-728-19	Sequence 19, Appl
39	536	70.9	135	1	US-08-474-040-19	Sequence 19, Appl
40	536	70.9	135	1	US-08-487-200-19	Sequence 19, Appl
41	536	70.9	135	2	US-08-303-569B-31	Sequence 31, Appl
42	536	70.9	135	3	US-08-484-537-19	Sequence 19, Appl
43	534	70.6	233	3	US-08-444-644-33	Sequence 33, Appl
44	534	70.6	233	3	US-08-232-246A-33	Sequence 33, Appl
45	534	70.6	235	3	US-08-444-644-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-253-877C-8
; Sequence 8, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-253-877C-8

Query Match 79.8%; Score 603; DB 1; Length 139;
Best Local Similarity 80.6%; Pred. No. 1.7e-49;
Matches 112; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366

FILING DATE: 03-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/187,407

FILING DATE: 27-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/990,542

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/493,299

FILING DATE: 14-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/324,392

FILING DATE: 14-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093

REFERENCE/DOCKET NUMBER: 8648.39USC1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-888-366-2

Query Match 77.4%; Score 585; DB 2; Length 116;

Best Local Similarity 93.3%; Pred. No. 6.7e-48;

Matches 112; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Qy 20 QVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRPGQGLEWIGWIYPGSGTNY 79

Db 1 EVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRPGQGLEWIGWIYPGSGTKY 60

Qy 80 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARGGNFPPSYAMDYWGQGTSTVSS 139

Db 61 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARGG----YAMDYWGQGTSTVSS 116

RESULT 5

PCT-US93-11612-4

Sequence 4, Application PC/TUS9311612

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11612

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 140 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-11612-4

Query Match 76.0%; Score 574.5; DB 5; Length 140;

Best Local Similarity 78.0%; Pred. No. 8.1e-47;

Matches 110; Conservative 14; Mismatches 14; Indels 3; Gaps 2;

Qy 1 MGWEIFLLSGTAGVHCVOLOQSGPELVKPGALVKISKASGYTFTSYDINWVKR 60

Db 1 MENSWIFLLSGTAGVHSEVQLQSGPDLVKPGASVMSCKASGYTFTSYMHVWKRP 60

Qy 61 GQGLEWIGWIYPGSGTNYNEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARG-- 118

Db 61 GQGLEWIGWIYPNDGTYNEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCAREY 120

Qy 119 GNFPYAMDYWGQGTSTVSS 139

Db 121 GNVVRY-FDVMGAGTTVTVSS 140

RESULT 6

US-07-634-278-69

Sequence 69, Application US/07634278

Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA: US 07/290,975
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-634-278-69

Query Match 75.3%; Score 569; DB 1; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MGMSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYTFTDYNHWVKQSH 60
QY 61 GQGLEWIGWYIPGCGTNTNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
DB 61 GKSLEWIGWYIPYNGGTGYNQKFKSKATLTVDNSSSTAYMDVRSLSSEDSAVYYCARG-- 118
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 7
US-08-477-728-69
; Sequence 69, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-728-69

Query Match 75.3%; Score 569; DB 1; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MGMSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISKASGYTFTDYNHWVKQSH 60
QY 61 GQGLEWIGWYIPGCGTNTNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
DB 61 GKSLEWIGWYIPYNGGTGYNQKFKSKATLTVDNSSSTAYMDVRSLSSEDSAVYYCARG-- 118
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 8
US-08-474-040-69
; Sequence 69, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-69

Query Match 75.3%; Score 569; DB 1; Length 135;

Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MGWRFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWRFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Qy 61 GQGLEWIGWIYPGDDGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120

Db 61 GQGLEWIGWIYPGDDGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120

Qy 121 FPSYAMDYWGQGTSTVTSS 139

Db 119 --RPAMDYWGQGTSTVTSS 135

RESULT 9

US-08-487-200-69

Sequence 69, Application US/08487200

Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,200

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-69

Query Match 75.3%; Score 569; DB 1; Length 135;

Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MGWRFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWRFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Qy 61 GQGLEWIGWIYPGDDGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120

Db 61 GQGLEWIGWIYPGDDGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGN 120

Qy 121 FPSYAMDYWGQGTSTVTSS 139

Db 119 --RPAMDYWGQGTSTVTSS 135

RESULT 10

US-08-484-537-69

Sequence 69, Application US/08484537

Patent No. 6180370

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,537

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

```

; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-537-69

Query Match 75.3%; Score 569; DB 3; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQSH 60

QY 61 GQGLEWIGIYPGDGGTNYNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GKSLWIGIYIPNGGTGYNQKFKSKATLTVDNSSSTAYMDVRLSLSSENSAVYFCARG-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 11
US-09-254-180C-143
; Sequence 143, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-254-180C-143

```

```

Query Match 74.8%; Score 565.5; DB 4; Length 138;
Best Local Similarity 77.0%; Pred. No. 5.6e-46;
Matches 107; Conservative 13; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWSWIFLLSVTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGIYPGDGGTNYNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGIYIPNGGTGYNQKFKSKATLTVDNSSSTAYMDVRLSLSSENSAVYFCARG-- 118

```

```

DB 61 GHGLEWIGIYLPGLTYNTYNEKFGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARYD 120
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 121 Y-DYAMDYWGQGTSTVTVSS 138

RESULT 12
US-08-579-378A-4
; Sequence 4, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: CO, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheut, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-4

```

```

Query Match 74.8%; Score 565.5; DB 3; Length 140;
Best Local Similarity 76.6%; Pred. No. 5.7e-46;
Matches 108; Conservative 15; Mismatches 15; Indels 3; Gaps 2;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGIYPGDGGTNYNEKFGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARG-- 118
DB 61 GQGLEWIGIYIPNGGTGYNQKFKSKATLTSDKSSSTAYMELSLTSEDSAVYFCARBEY 120

QY 119 GNFPSPYAMDYWGQGTSTVTVSS 139
DB 119 GNFPSPYAMDYWGQGTSTVTVSS 139

```


; Sequence 85, Application US/08474040

; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-040-85

Query Match 74.3%; Score 561.5; DB 1; Length 138;
Best Local Similarity 77.0%; Pred. No. 1.3e-45;
Matches 107; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MGRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISCKASGYFTSYDINWVKQRP 60
Db 1 MGRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISCKASGYFTSYDINWVKQSH 60

Qy 61 GQGLEWIGWYPGDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
Db 61 GQNLWIGLINFYNGGTSYNGKFKGKATLTVDKSSNTAYMQLSSLTSENSAVYCTTRG- 119

Qy 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 FRDYSMDYWGQGTSTVTVSS 138

Search completed: May 25, 2005, 15:58:25
Job time : 18.3265 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 64.134 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773a-13

Perfect score: 756

Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NPFYAMDYWGQTSVTSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	756	100.0	139	13	US-10-006-773-13
2	678.5	89.7	138	8	US-08-779-784-31
3	678.5	89.7	138	14	US-10-010-729-67
4	569	75.3	135	15	US-10-389-155-60
5	569	75.3	135	15	US-10-389-417-60
6	569	75.3	135	15	US-10-452-357-69
7	563.5	74.5	136	14	US-10-138-505-12
8	563.5	74.5	136	15	US-10-257-864A-88
9	563.5	74.5	136	15	US-10-221-131-93
10	563.5	74.5	136	15	US-10-399-518-117
11	561.5	74.3	136	14	US-10-138-505-8
12	561.5	74.3	136	15	US-10-257-864A-86
13	561.5	74.3	136	15	US-10-221-131-91

14	561.5	74.3	136	15	US-10-399-518-115	Sequence 115, Appl
15	561.5	74.3	138	15	US-10-389-155-72	Sequence 72, Appl
16	561.5	74.3	138	15	US-10-389-417-72	Sequence 72, Appl
17	561.5	74.3	138	15	US-10-452-357-85	Sequence 85, Appl
18	558	73.8	118	11	US-09-926-323-2	Sequence 2, Appli
19	555.5	73.5	140	14	US-10-283-349-27	Sequence 27, Appl
20	548	72.5	137	15	US-10-462-062-153	Sequence 153, App
21	548	72.5	137	15	US-10-462-062-154	Sequence 154, App
22	542	71.7	135	14	US-10-244-821-91	Sequence 91, Appl
23	541	71.6	467	17	US-10-500-696-2	Sequence 2, Appli
24	540.5	71.5	438	9	US-09-903-327A-6	Sequence 6, Appli
25	540.5	71.5	456	9	US-09-903-327A-2	Sequence 13, Appl
26	540.5	71.5	493	9	US-09-903-327A-13	Sequence 12, Appl
27	540.5	71.5	510	9	US-09-903-327A-12	Sequence 14, Appl
28	540.5	71.5	597	9	US-09-903-327A-11	Sequence 19, Appl
29	540.5	71.5	613	9	US-10-452-357-19	Sequence 40, Appl
30	540	71.4	135	15	US-10-682-845-40	Sequence 40, Appl
31	538.5	71.2	138	16	US-10-682-845-40	Sequence 40, Appl
32	538.5	71.2	143	14	US-10-010-729-66	Sequence 66, Appl
33	537	71.0	139	17	US-10-687-035-34	Sequence 34, Appl
34	536	70.9	135	15	US-10-389-155-32	Sequence 32, Appl
35	536	70.9	135	15	US-10-389-417-32	Sequence 32, Appl
36	532.5	70.4	138	9	US-09-753-436-78	Sequence 78, Appl
37	532.5	70.4	138	14	US-10-163-942-78	Sequence 7, Appli
38	531.5	70.3	136	16	US-10-768-193-7	Sequence 7, Appli
39	531.5	70.3	468	10	US-09-795-515-7	Sequence 7, Appli
40	531.5	70.3	468	15	US-10-704-352-7	Sequence 7, Appli
41	531.5	70.3	468	15	US-10-704-071-7	Sequence 7, Appli
42	531.5	70.3	468	16	US-10-682-845-38	Sequence 38, Appl
43	529.5	70.0	132	14	US-10-197-080-2	Sequence 2, Appli
44	529.5	70.0	132	17	US-10-484-031-2	Sequence 2, Appli
45	529.5	70.0	140	9	US-09-748-960-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-006-773-13
; Sequence 13, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jughans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-13

Query Match 100.0%; Score 756; DB 13; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP	60
Db	1	MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP	60
Qy	61	GGGLEWIGWYIPGOGGTYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN	120
Db	61	GGGLEWIGWYIPGOGGTYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN	120
Qy	121	FPYAMDYWGQTSVTSS	139
Db	121	FPYAMDYWGQTSVTSS	139

RESULT 2
US-08-779-784-31
; Sequence 31, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-31

Query Match 89.7%; Score 678.5; DB 8; Length 138;
Best Local Similarity 92.1%; Pred. No. 1.8e-52;
Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
QY 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
QY 121 FPSYAMDYWGQTSVTSS 139
DB 121 FYWY-FDVGAGTTVTSS 138

RESULT 3
US-08-779-784-31
; Sequence 31, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-31

Query Match 89.7%; Score 678.5; DB 8; Length 138;
Best Local Similarity 92.1%; Pred. No. 1.8e-52;
Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
QY 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
QY 121 FPSYAMDYWGQTSVTSS 139
DB 121 FYWY-FDVGAGTTVTSS 138

RESULT 3
US-08-779-784-31
; Sequence 31, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-779-784-31

US-10-010-729-67
; Sequence 67, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IGM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-67

Query Match 89.7%; Score 678.5; DB 14; Length 138;
Best Local Similarity 92.1%; Pred. No. 1.8e-52;
Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKRQP 60
QY 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
QY 121 FPSYAMDYWGQTSVTSS 139
DB 121 FYWY-FDVGAGTTVTSS 138

RESULT 4
US-10-389-155-60
; Sequence 60, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-155-60

```

```

Query Match      75.3%; Score 569; DB 15; Length 135;
Best Local Similarity 77.7%; Pred. No. 8.8e-43;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MGWEIFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGWEIFLLSAGTAGVHSEVLOQSGPELVKPGASVKISKASGYTTTDYNMHWVKQSH 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 GQGLEWIGIYIPGOGGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGGN 120
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GKSLEWIGIYIPYNGGTGYNOKFKSKATLTVDNSSSTAYMDVRSLSLTSSEDSAVYVCARG-- 118
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 121 FPSYAMDYWGQGTSTVTSS 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 --RPAMDYWGQGTSTVTSS 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 5
US-10-389-417-60
; Sequence 60, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
;               Co, Man Sung
;               Schneider, William P.
;               Landolfi, Nicholas F.
;               Coelingh, Kathleen L.
;               Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,417
; FILING DATE: 13-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-417-60

Query Match      75.3%; Score 569; DB 15; Length 135;
Best Local Similarity 77.7%; Pred. No. 8.8e-43;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MGWEIFLLSAGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGWEIFLLSAGTAGVHSEVLOQSGPELVKPGASVKISKASGYTTTDYNMHWVKQSH 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 GQGLEWIGIYIPGOGGTNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCARGGN 120
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GKSLEWIGIYIPYNGGTGYNOKFKSKATLTVDNSSSTAYMDVRSLSLTSSEDSAVYVCARG-- 118
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 121 FPSYAMDYWGQGTSTVTSS 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 --RPAMDYWGQGTSTVTSS 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-10-452-357-69
; Sequence 69, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William
; APPLICANT: Landolfi, Nicholas
; APPLICANT: Coelingh, Kathleen
; APPLICANT: Selick, Harold
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; FILE REFERENCE: 05882.0078.CNUS01
; CURRENT APPLICATION NUMBER: US/10/452,357
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/718,993
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/487,200
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/634,278

```



```
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pGEM-M2H
US-10-221-131-93

Query Match      74.5%; Score 563.5; DB 15; Length 136;
Best Local Similarity 77.0%; Pred. No. 2.7e-42;
Matches 107; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCVQLQSGPGLVKGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHQSQVQLQSGPGLVKGASVKMSCKASGYTFANHHVWKQKP 60

Qy 61 GQGLEWIGWYIPGPGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKDKATLTSDKSSSTAYMDLSSLSAEDSAVYYCARGG- 119

Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGGTTLTVSS 136

RESULT 10
US-10-399-518-117
; Sequence 117, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIOHKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-399-518-117

Query Match      74.5%; Score 563.5; DB 15; Length 136;
Best Local Similarity 77.0%; Pred. No. 2.7e-42;
Matches 107; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCVQLQSGPGLVKGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHQSQVQLQSGPGLVKGASVKMSCKASGYTFANHHVWKQKP 60

Qy 61 GQGLEWIGWYIPGPGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKDKATLTSDKSSSTAYMDLSSLSAEDSAVYYCARGG- 119

Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGGTTLTVSS 136

RESULT 11
US-10-138-505-8
; Sequence 8, Application US/10138505
; Publication No. US20030108546A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: OH-EDA, Masayoshi
; APPLICANT: KIKUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/10/138,505
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-138-505-8

Query Match      74.3%; Score 561.5; DB 14; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCVQLQSGPGLVKGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHQSQVQLQSGPGLVKGASVKMSCKASGYTFANHHVWKQKP 60

Qy 61 GQGLEWIGWYIPGPGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKGKATLTSEKSSAAAYMELSLSEDSAVYYCARGG- 119

Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGGTTLTVSS 136

RESULT 12
US-10-257-864A-86
; Sequence 86, Application US/10257864A
; Publication No. US20040059393A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; APPLICANT: GOTEMBA-SHI, OHTOMO
; TITLE OF INVENTION: AGONIST ANTIBODIES
; FILE REFERENCE: 065678-0107
; CURRENT APPLICATION NUMBER: US/10/257,864A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: JP2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP2000-321821
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: JP2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
```

```
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence encoded by SEQ ID NO: 6
US-10-257-864A-86

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 13
US-10-221-131-91
; Sequence 91, Application US/10221131
; Publication No. US20040073013A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOHSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pGEM-M1H
US-10-221-131-91

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 14
US-10-399-518-115
; Sequence 115, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-399-518-115

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 15
US-10-389-155-72
; Sequence 72, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/389,155
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
```

```
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence encoded by SEQ ID NO: 6
US-10-257-864A-86

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 13
US-10-221-131-91
; Sequence 91, Application US/10221131
; Publication No. US20040073013A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOHSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pGEM-M1H
US-10-221-131-91

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 14
US-10-399-518-115
; Sequence 115, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-399-518-115

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSGTAGVHSQVQLQQSGPDLVPGASVKMSCKASGYTFVNHVHWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GQGLEWIGWIYPDGGTNNYNEKFGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGWIYPNDGTYNEKFGKATLTSEKSSAAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   |.:|:|||||:|.

RESULT 15
US-10-389-155-72
; Sequence 72, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/389,155
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
```


Search completed: May 25, 2005, 16:06:52
Job time : 65.259 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 19.654 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773A-13
Perfect score: 756
Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NFRSYAMDYWGQTSVTSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	82.3	117	1 HWMSA1	Ig heavy chain pre
2	613	81.1	469	2 S37483	Ig gamma-2a chain
3	597.5	79.0	138	2 S21810	Ig heavy chain V r
4	564.5	74.7	140	2 PH1482	Ig heavy chain V r
5	562.5	74.4	140	1 HWMSG7	Ig heavy chain pre
6	560	74.1	139	2 A27609	Ig heavy chain pre
7	557.5	73.7	138	2 E32513	Ig heavy chain pre
8	547	72.4	474	1 G2MS11	Ig gamma-2b chain
9	544.5	72.0	140	2 PH1489	Ig heavy chain V r
10	544.5	72.0	246	2 S38950	Ig gamma chain - m
11	544.5	72.0	446	2 S40295	Ig gamma-2a chain
12	542.5	71.8	140	2 PH1486	Ig heavy chain V r
13	542.5	71.8	140	2 PH1498	Ig heavy chain V r
14	539.5	71.4	135	2 PH1492	Ig heavy chain V r
15	539.5	71.4	135	2 PH1493	Ig heavy chain V r
16	536.5	71.0	140	2 PH1484	Ig heavy chain V r
17	536	70.9	139	2 PS0024	Ig heavy chain pre
18	533	70.5	137	2 H32513	Ig heavy chain pre
19	532.5	70.4	137	2 PH1488	Ig heavy chain V r
20	530.5	70.2	140	2 PH1483	Ig heavy chain V r
21	529.5	70.0	140	2 T01407	Ig heavy chain (my
22	529	70.0	135	2 A30577	Ig heavy chain pre
23	526	69.6	139	1 MHMS18	Ig heavy chain pre
24	524.5	69.4	140	2 A36194	Ig heavy chain V r
25	524	69.3	140	2 S09216	Ig heavy chain pre
26	523	69.2	475	2 S01321	Ig gamma-2b chain
27	522.5	69.1	135	2 PH1494	Ig heavy chain V r
28	522	69.0	141	2 JL0076	Ig heavy chain pre
29	521	68.9	141	2 A39276	Ig heavy chain pre

RESULT 1

HWMSA1

Ig heavy chain precursor V region (A1/A4) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C;Accession: A02029

R;Yancopoulos, G.D.; Alt, F.W.

Cell 40, 271-281, 1995

A;Title: Developmentally controlled and tissue-specific expression of unrearranged V-H 9

A;Reference number: A90860; MUID:85099340; PMID:2578321

A;Accession: A02029

A;Molecule type: DNA

A;Residues: 1-117 <YAN>

A;Cross-references: UNIPROT:P06327; GB:M13787; NID:gl96006; PIDN:AAA38499.1; PID:g466291

A;Note: the sequence was determined from the germline gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <MAT>

F;20-49/Region: framework 1

F;34-117/Domain: immunoglobulin homology <IMM>

F;50-54/Region: complementarity-determining 1

F;55-68/Region: framework 2

F;69-85/Region: complementarity-determining 2

F;86-117/Region: framework 3

F;41-115/Disulfide bonds: #status predicted

Query Match 82.3%; Score 622; DB 1; Length 117;

Best Local Similarity 98.3%; Pred. No. 5.2e-46;

Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSVDINVKORP 60

Db 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSVDINVKORP 60

Qy 61 GQGLEWIGWIYPGGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCAR 117

Db 61 GQGLEWIGWIYPGGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCAR 117

RESULT 2

S37483

Ig gamma-2a chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37483

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37483

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
A;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 613; DB 2; Length 469;
Best Local Similarity 80.6%; Pred. No. 1.2e-44;
Matches 112; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLRWIGWYIPASGNTKYNEFKGKATLTVDTSSTAYMQLSSLTSEDTAVYFCARWG 120

QY 121 FPSYAMDYWGQTSVTSS 139
DB 121 ATATLDYWGQTTLTSS 139

RESULT 3
S21810
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21810
R;Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain
A;Reference number: S21810
A;Accession: S21810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <OST>
A;Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164
C;Genetics:
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 597.5; DB 2; Length 138;
Best Local Similarity 83.6%; Pred. No. 7.3e-44;
Matches 117; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYIPGNVNTKYNEFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR--N 118

QY 121 FPSYAMDYWGQTSVTSS 139
DB 119 YGSSYGLAYWGQTLTVSA 138

RESULT 4
PH1482
Ig heavy chain V region (clones 36-35[IG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have a for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1482

A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 564.5; DB 2; Length 140;
Best Local Similarity 77.6%; Pred. No. 4.7e-41;
Matches 111; Conservative 10; Mismatches 15; Indels 7; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117
DB 61 GQGLEWIGWYIPNGYTKYNEFKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSVY 120

QY 118 -CGNFPYSAMDYWGQTSVTSS 139
DB 121 YGG---SYVFDYWGQTTLTSS 140

RESULT 5
HVM5G7
Ig heavy chain precursor V region (93G7, 36-65) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A94261; A02028
R;Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain
A;Reference number: A94264; MUID:82152818; PMID:6801765
A;Accession: A94264
A;Molecule type: mRNA
A;Residues: 1-140 <SIM>
A;Cross-references: UNIPROT:P01746; GB:J00493; NID:g195006; PIDN:AAA38128.1; PID:g19500
A;Experimental source: strain A/J, hybridoma 93G7
R;Siekevitz, M.; Geffer, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Eur. J. Immunol. 12, 1023-1032, 1982
A;Title: The genetic basis of antibody production: the dominant anti-arsenate idiotype
A;Reference number: A91261; MUID:83131846; PMID:6186498
A;Accession: A91261
A;Molecule type: DNA
A;Residues: 20-76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>
A;Cross-references: GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:g196202
A;Experimental source: strain A/J, hybridoma 36-65
A;Note: the sequence was determined from the differentiated gene
A;Note: from analysis of the sizes of several other differentiated genes that hybridize
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 74.4%; Score 562.5; DB 1; Length 140;
Best Local Similarity 77.6%; Pred. No. 6.9e-41;
Matches 111; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117
DB 61 GQGLEWIGWYIPNGYTKYNEFKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSHY 120

Db 61 GQGLEWIGNIYPCSSSTNYNEKPKSKATLTVDTSSTAYNQLSLSDSSAVVYCAR-RL 119

Qy 121 FPSYAMDYWGQGTSTVTSS 139
: |||||

Db 120 YRYAMDYWGQGTSTVTSS 138

RESULT 8

G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Nierbach, M.; Munsiker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific r
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <F10>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54822
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Ohta, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
R;Ollio, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: Immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul
F;157-222/Domain: immunoglobulin homology <IMI>

F;236-257/Region: hinge
 F;281-350/Domain: immunoglobulin homology <IM2>
 F;387-454/Domain: immunoglobulin homology <IM3>
 F;152/Disulfide bonds: interchain (to light chain) #status predicted
 F;164-220,288-348,394-452/Disulfide bonds: #status predicted
 F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.0%; Score 544.5; DB 1; Length 474;
 Best Local Similarity 74.8%; Pred. No. 4.7e-39;
 Matches 103; Conservative 17; Mismatches 17; Indels 2; Gaps 1;

QY 1 MGRWIFLFLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 DB 1 MGRWIFLFLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWIPGDDGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
 DB 61 GQGLEWIGWIPGDDGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120

QY 121 FPSYAMDYWGQGTSTVTVSS 139
 DB 121 YDWEFA--YWGQGTSTVTVSS 137

RESULT 9
 PH1489
 Ig heavy chain V region (clone X41-2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1489
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993
 A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have a for somatic mutation.
 A:Reference number: PH1482; PMID:93171820; PMID:8436910
 A:Accession: PH1489
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-140 <GIU>
 A:Experimental source: hybridoma cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 544.5; DB 2; Length 140;
 Best Local Similarity 74.8%; Pred. No. 2.3e-39;
 Matches 107; Conservative 12; Mismatches 17; Indels 7; Gaps 2;

QY 1 MGRWIFLFLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
 DB 1 MGRWIFLFLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWIPGDDGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117
 DB 61 GQGLEWIGWIPGDDGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117

QY 118 -GNFSPYAMDYWGQGTSTVTVSS 139
 DB 121 YGG---SYVPDYWGQGTSTVTVSS 140

RESULT 10
 S38950
 Ig gamma chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S38950
 R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
 A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
 A:Reference number: S38950; PMID:94128242; PMID:8297501
 A:Accession: S38950

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-246 <KLE>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;137-201/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 544.5; DB 2; Length 246;
 Best Local Similarity 85.8%; Pred. No. 4e-39;
 Matches 103; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 20 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWIPGDDGTYN 79
 DB 1 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWIPGDDGTYN 79

QY 80 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGNPSPVAMDYWGQGTSTVTVSS 139
 DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGNPSPVAMDYWGQGTSTVTVSS 117

RESULT 11
 S40295
 Ig gamma-2a chain (mAb735) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C:Accession: S40295
 R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
 A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
 A:Reference number: S40295
 A:Accession: S40295
 A:Molecule type: protein
 A:Residues: 1-446 <KLE>
 A:Cross-references: UNIPROT:Q99L25
 C:Genetics:
 A:Map position: 12
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
 F;1-446/Product: Ig gamma-2a chain #status experimental <MAI>
 F;1-117/Domain: V-D-J region <VDJ>
 F;118-446/Domain: C region <CHR>
 F;215-230/Region: hinge
 F;231-340/Domain: C2 region <CH2>
 F;341-446/Domain: C3 region <CH3>
 F;360-427/Domain: immunoglobulin homology <IMM>
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
 F;132/Disulfide bonds: interchain (to light chain) #status predicted
 F;224,227,229/Disulfide bonds: interchain #status predicted
 F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 72.0%; Score 544.5; DB 2; Length 446;
 Best Local Similarity 85.8%; Pred. No. 7.2e-39;
 Matches 103; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 20 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWIPGDDGTYN 79
 DB 1 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWIPGDDGTYN 60

QY 80 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGNPSPVAMDYWGQGTSTVTVSS 139
 DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGNPSPVAMDYWGQGTSTVTVSS 117

RESULT 12
 PH1486
 Ig heavy chain V region (clone X7-3D12) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1486
 R:Giusti, A.M.; Manser, T.
 J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1486

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 542.5; DB 2; Length 140;

Best Local Similarity 76.2%; Pred. No. 3.4e-39;

Matches 109; Conservative 9; Mismatches 18; Indels 7; Gaps 2;

Qy 1 MGWRWIFLLSGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVQLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGYINYNKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 118 -GGNPPSYAMDYWGQGTSTVSS 139

Db 121 YGG---SYFDYWGQGTSLTVSS 140

RESULT 13

PH1498

Ig heavy chain V region (clone X7-4G7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1498

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1498

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 542.5; DB 2; Length 140;

Best Local Similarity 75.5%; Pred. No. 3.4e-39;

Matches 108; Conservative 10; Mismatches 18; Indels 7; Gaps 2;

Qy 1 MGWRWIFLLSGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVQLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 116

Db 61 GQGLEWIGYINPGNGYINYNKFKGKTLTADKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 117 RGNPPSYAMDYWGQGTSTVSS 139

Db 121 YGG---SYFDYWGQGTSLTVSS 140

RESULT 14

PH1492

Ig heavy chain V region (clone PH11-4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1492

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1492

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

F:79/Region: ochre stop codon

Query Match 71.4%; Score 539.5; DB 2; Length 135;

Best Local Similarity 76.8%; Pred. No. 6e-39;

Matches 106; Conservative 10; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MGWRWIFLLSGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVQLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGYITKDEKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSLY 120

Qy 118 -GGNPPSYAMDYWGQGTST 134

Db 121 YGG---SYAFDYWGQGT 135

RESULT 15

PH1493

Ig heavy chain V region (clone PH14-3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1493

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1493

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 539.5; DB 2; Length 135;

Best Local Similarity 76.1%; Pred. No. 6e-39;

Matches 105; Conservative 11; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MGWRWIFLLSGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVQLOQSGAELVRAGSSVVMKSCASGYTFTTGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGFTKYNEKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 118 -GGNPPSYAMDYWGQGTST 134

Db 121 YGG---SYFDYWGQGT 135

Search completed: May 25, 2005, 16:48:40

Job time : 20.654 secs

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057672; AAH57672.1; -;
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00395; IG_LIKE; 4.
DR PROSITE; PS00290; IG_LIKE; 4.
DR PROSITE; PS00290; IG_LIKE; 4.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;

Query Match 74.7%; Score 564.5; DB 2; Length 464;
Best Local Similarity 78.4%; Pred. No. 1.1e-47;
Matches 109; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPGLVPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPGLVPGALVKISCKASGYTFTSYDINWVKQRS 60

QY 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARGN 120
DB 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARGN 118

QY 121 FPSYANDYWGQTSVTSS 139
DB 119 ---YDALYWGQTSVTSS 134

RESULT 6
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -/- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00493; AAA38128.1; -;
DR PIR; A94264; HVMG7.
DR HSSP; P01747; 1JFQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00395; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 Ig heavy chain V region 93G7.
FT DOMAIN 20 139 Ig-like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 74.4%; Score 562.5; DB 1; Length 140;
Best Local Similarity 77.6%; Pred. No. 4.5e-48;
Matches 111; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPGLVPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPGLVPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCAR--- 117
DB 61 GQGLEWIGWYFGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARSHY 120

QY 118 -GQNFPSYANDYWGQTSVTSS 139
DB 121 YGG---SYDFDYWGQTSVTSS 140

RESULT 7
Q7TWT6 PRELIMINARY; PRT; 614 AA.
ID Q7TWT6
AC Q7TWT6;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE MGC0843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 : Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 67.7544 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773A-13
Perfect score: 756
Sequence: 1 MGWRWIFLFLSLGTVAGVHCQ.....NFPSYAMDYWGQTSVTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630.5	83.4	481	Q91WT1	Q91wt1 mus musculus
2	625.5	82.7	480	Q8K0Z4	Q8k0z4 mus musculus
3	622	82.3	117	HV52_MOUSE	P06327 mus musculus
4	578.5	76.5	473	Q9D8L4	Q9d8l4 mus musculus
5	564.5	74.7	464	Q6PF95	Q6pf95 mus musculus
6	562.5	74.4	140	HV02_MOUSE	P01746 mus musculus
7	555.5	73.5	614	Q7TMT6	Q7tmt6 mus musculus
8	555	73.4	465	Q6PJB2	Q6pjb2 mus musculus
9	549	72.6	463	Q99LC4	Q99lc4 mus musculus
10	542	71.7	488	Q91WR1	Q91wr1 mus musculus
11	541.5	71.6	472	Q6FJA7	Q6fja7 mus musculus
12	540	71.4	613	Q8VCX7	Q8vcx7 mus musculus
13	538	71.2	482	Q8K172	Q8k172 mus musculus
14	529.5	70.0	168	Q8VDC9	Q8vdc9 mus musculus
15	526	69.6	139	HV07_MOUSE	P01751 mus musculus
16	525.5	69.5	470	Q7TMK1	Q7tmk1 mus musculus
17	516.5	68.3	489	Q8VCX4	Q8vcx4 mus musculus
18	514	68.0	488	Q8K0F2	Q8k0f2 mus musculus
19	509	67.3	117	HV14_MOUSE	P01758 mus musculus
20	501	66.3	487	Q65ZL2	Q65zl2 mus sp. fv/
21	497.5	65.8	142	Q924Q1	Q924q1 mus musculus
22	496	65.6	137	HV11_MOUSE	P01755 mus musculus
23	494.5	65.4	138	HV48_MOUSE	P03980 mus musculus
24	494.5	65.4	474	Q8R3H6	Q8r3h6 mus musculus
25	492	65.1	145	Q924R1	Q924r1 mus musculus
26	492	65.1	145	Q924R4	Q924r4 mus musculus
27	490	64.8	145	Q924Q6	Q924q6 mus musculus
28	490	64.8	481	Q8VCV5	Q8vcv5 mus musculus
29	489.5	64.7	146	Q924Q3	Q924q3 mus musculus
30	489	64.7	145	Q924Q9	Q924q9 mus musculus
31	487	64.4	143	Q924R0	Q924r0 mus musculus

32	487	64.4	145	2	Q924P7	Q924p7 mus musculus
33	486.5	64.4	147	2	Q92583	Q92583 mus musculus
34	485.5	64.2	120	1	HV03_MOUSE	P01747 mus musculus
35	483	63.9	143	2	Q924Q0	Q924q0 mus musculus
36	480	63.5	117	1	HV04_MOUSE	P01748 mus musculus
37	478.5	63.3	140	2	Q924E2	Q924e2 mus musculus
38	475.5	62.9	117	2	Q9QXE9	Q9qxe9 mus musculus
39	475	62.8	117	1	HV06_MOUSE	P01750 mus musculus
40	474.5	62.8	134	2	Q65ZR6	Q65zr6 mus musculus
41	474	62.7	145	2	Q924Q7	Q924q7 mus musculus
42	472.5	62.5	140	2	Q924P8	Q924p8 mus musculus
43	469	62.0	117	1	HV05_MOUSE	P01749 mus musculus
44	468.5	62.0	146	2	Q924E8	Q924e8 mus musculus
45	465	61.5	111	2	Q9D9B8	Q9d9b8 mus musculus

ALIGNMENTS

RESULT 1

ID	Q91WT1	PRELIMINARY;	PRT;	481 AA.
AC	Q91WT1;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Igh-VJ558 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RX	MEDLINE=2338257; PubMed=1247732; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
[2]				
RC	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC013490; AAH13490.1; -			
DR	HSSP; P01751; 1A6W.			
DR	Pfam; PF07654; Cl-aet; 2.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.			
SQ	SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;			

Query Match 83.4%; Score 630.5; DB 2; Length 481;
Best Local Similarity 85.6%; Pred No. 3e-54;
Matches 119; Conservative 5; Mismatches 12; Indels 3; Gaps 1;
Qy 1 MGWRWIFLFLSLGTVAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKRP 60

Db 1 MGRWIFLLSGTAGVQCQVQLQSGPELVKPGASVKISCKASGYTFTSYIHWKQRP 60
QY 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
Db 61 GQGLVWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 119
QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --GWAFDYWGQGTSTVTVSS 136

RESULT 2
Q8K0Z4 PRELIMINARY; PRT; 480 AA.
ID Q8K0Z4
AC Q8K0Z4
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC029188; AAH29188.1; -;
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C69CDBED CRC64;

Query Match 82.7%; Score 625.5; DB 2; Length 480;
Best Local Similarity 84.4%; Pred. No. 9.4e-54;
Matches 119; Conservative 6; Mismatches 9; Indels 7; Gaps 2;
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
Db 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARG-- 118
Db 61 GQGPWIGWISFDGSSSEYNEKFKGKATLTADKSSNTAYMQLSSLTSENSAVYFCARSKL 120
QY 119 GNFPYSAMDYWGQGTSTVTVSS 139
Db 121 GGFA-----YWGQGTSTVTVSA 136

RESULT 3
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RA Yancopoulos G.D., Alt F.W.;
RT "developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC EMBL; M13787; AAA38499.1; -;
DR FIR; A02029; HVMSAL.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region VH58 A1/A4.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 82.3%; Score 622; DB 1; Length 117;
Best Local Similarity 98.3%; Pred. No. 4.3e-54;
Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
Db 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
QY 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
Db 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117

RESULT 4
Q9D8L4

```
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAHS3409.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 73.5%; Score 555.5; DB 2; Length 614;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
Matches 111; Conservative 6; Mismatches 21; Indels 1; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKORP 60
DB 1 MEWPCIFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKORP 60

QY 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 121 --SSRYFAWYGQGLTVTSSA 138

RESULT 8
Q6PJB2
ID Q6PJB2 PRELIMINARY; PRT; 465 AA.
AC Q6PJB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4B8DB3E21 CRC64;

Query Match 73.4%; Score 555; DB 2; Length 465;
Best Local Similarity 76.3%; Pred. No. 9.7e-47;
Matches 106; Conservative 12; Mismatches 17; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKORP 60
DB 1 MGWGVFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKORP 60

QY 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --YVFDYWGQGLTVTSS 135

RESULT 9
Q99LC4
ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-4 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```

RT and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR FJ; B45837; B45837.
DR HSP; P01869; ICL7.
DR MGD; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte. .; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 463 AA; 51007 MW; EA674C6BBC30783 CRC64;

Query Match 72.6%; Score 549; DB 2; Length 463;
Best Local Similarity 74.1%; Pred. No. 3.8e-46;
Matches 103; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGRWIFLLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWIFLLSLGTAGVHSGVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYIPGSGNTYSEKFKGKATLTADKSSSTAYMHLSSLTSENSAVYFCARSSV 120

QY 121 FPSYANDYWGQTSVTSS 139
DB 121 YSYDLFAYWGQGLTVTSA 139

RESULT 10
Q91WR1 PRELIMINARY; PRT; 488 AA.
ID Q91WR1
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR FJ; B45837; B45837.
DR HSP; P01869; ICL7.
DR MGD; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte. .; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 463 AA; 51007 MW; EA674C6BBC30783 CRC64;

Query Match 72.6%; Score 549; DB 2; Length 463;
Best Local Similarity 74.1%; Pred. No. 3.8e-46;
Matches 103; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGRWIFLLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWIFLLSLGTAGVHSGVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYIPGSGNTYSEKFKGKATLTADKSSSTAYMHLSSLTSENSAVYFCARSSV 120

QY 121 FPSYANDYWGQTSVTSS 139
DB 121 YSYDLFAYWGQGLTVTSA 139

RESULT 10
Q91WR1 PRELIMINARY; PRT; 488 AA.
ID Q91WR1
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -.
DR HSP; P01751; IAGW.
DR MGD; MGI:96486; Igh-VJ558.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 488 AA; 52964 MW; F13068460B400B9D CRC64;

Query Match 71.7%; Score 542; DB 2; Length 488;
Best Local Similarity 72.0%; Pred. No. 2e-45;
Matches 103; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

QY 1 MGRWIFLLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGRWIFLLSLGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGWYIPGSGNTYSEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

QY 121 FPSYANDYWGQTSVTSS 139
DB 121 YSYDLFAYWGQGLTVTSA 139

RESULT 11
Q6PJA7 PRELIMINARY; PRT; 472 AA.
ID Q6PJA7
AC Q6PJA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

```

```
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
DR EMBL; BC018535; AAH18535.1; -
DR HSSP; P01865; IKES.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_Y.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 52299 MW; 165169C23D5D54B CRC64;

Query Match 71.6%; Score 541.5; DB 2; Length 472;
Best Local Similarity 73.2%; Pred. No. 2.2e-45;
Matches 104; Conservative 16; Mismatches 19; Indels 3; Gaps 2;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
D 1 MGWSWIFLLSGTAGVLSVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
QY 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGG- 119
D 61 GKSLEWIGWIYPNGGNGYKFKGKATLTVDKSSSTAYMELRLSLTSDSAVYVCARGY 120
QY 120 NPPSY--AMDYWGQGTSTVTVSS 139
D 121 SYTSYDHYFDYWGQGTSTVTVSS 142

RESULT 12
Q8VCX7
AC Q8VCX7; PRELIMINARY; PRT; 613 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AAH28249.1; -;
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;
Query Match 71.2%; Score 538; DB 2; Length 482;
Best Local Similarity 75.5%; Pred. No. 5e-45;
Matches 105; Conservative 9; Mismatches 23; Indels 2; Gaps 1;
QY 1 MGRWIFLLSCTAGVHCQVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
Db 1 MGWSCIIMFLAATATGTVHSGVQLQQFGAELVKGASVKLSCKASGYTFTSYDINWVKQRP 60
QY 61 GQGLEWIGWTPYDGGTNNYNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKATLTVDPSSTAYMQLSSLTSENSAVYCTREGD 120
QY 121 FPSYANDYWGQGTSTVTVSS 139
Db 121 YD--AMDYWGQGTSTVTVSS 137
RESULT 14
Q8VDC9 PRELIMINARY; PRT; 168 AA.
AC Q8VDC9;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Anti-MOG Z12 variable gamma 2a (Fragment).
GN Name-IgG2a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembli P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416332; CAC94867.1; -;
DR HSSP; P01863; 1E4W.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 168 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
Query Match 70.0%; Score 529.5; DB 2; Length 168;
Best Local Similarity 74.1%; Pred. No. 1.1e-44;
Matches 103; Conservative 11; Mismatches 24; Indels 1; Gaps 1;
QY 1 MGRWIFLLSCTAGVHCQVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
Db 1 MEWTVFLLSVTAGVHSGVQLQQSGAELMKGASVKISCKATGTFSSYDINWVKQRP 60
QY 61 GQGLEWIGWTPYDGGTNNYNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
Db 61 GHGLEWIGELPESGRTNNEKFKGKTFTADTSNTAYIQFSSLTSEDSAVYICANYGS 120
QY 121 FPSYANDYWGQGTSTVTVSS 139
Db 121 SRWY-FDVGAGTTVTVSS 138
RESULT 15
HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
CC Cell 24:623-637(1981).
CC -!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
CC making antibodies to the haptens (4-hydroxy-3-nitrophenyl)acetyl
CC (NPb antibodies).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch).

```
-----
CC  EMBL; J00529; AAA38170.1; -.
CR  PIR; A90809; MHMS18.
DR  PDB; 1A6U; X-ray; H=20-139.
DR  PDB; 1A6V; X-ray; H/I/J=20-139.
DR  PDB; 1A6W; X-ray; H=20-139.
DR  PDB; 1A6X; X-ray; H=20-139.
DR  PDB; 1A6Y; X-ray; A/C=20-139.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; IG; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  3D-structure; Immunoglobulin V region; Signal.
FT  SIGNAL 1
FT  CHAIN 20 139
FT  DOMAIN 20 49
FT  DOMAIN 50 54
FT  DOMAIN 55 68
FT  DOMAIN 69 85
FT  DOMAIN 86 117
FT  DOMAIN 118 124
FT  DOMAIN 125 139
FT  DISULFID 41 115
FT  STRAND 22 24
FT  STRAND 28 31
FT  TURN 33 34
FT  STRAND 37 44
FT  HELIX 48 50
FT  STRAND 52 58
FT  TURN 60 61
FT  STRAND 64 70
FT  TURN 72 74
FT  STRAND 77 79
FT  HELIX 81 83
FT  TURN 84 86
FT  STRAND 87 92
FT  TURN 93 96
FT  STRAND 97 102
FT  HELIX 107 109
FT  STRAND 111 118
FT  TURN 120 123
FT  STRAND 129 129
FT  STRAND 133 137
FT  NON_TER 139 139
SQ  SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 69.6%; Score 526; DB 1; Length 139;
Best Local Similarity 73.4%; Pred. No. 1.9e-44;
Matches 102; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MGWSCIMLFLLAATATGVHSQVLOQPGAEVLKPGASVKLSKASGYTFTSYMHWVKORP 60

Qy 61 GQGLEWIGWYPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGN 120
Db 61 GRGLEWIGRIDPNSGGTYNEKFKSKATLTVDKPSSTAYMQLSSLTSSEDSAVYVCARYDY 120

Qy 121 FPSYAMDYWGQGTSTVTVSS 139
Db 121 YGSSYFDYWGQGTTLTVSS 139
```

Search completed: May 25, 2005, 15:56:06
Job time : 68.7544 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 62.1321 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773A-15

Perfect score: 686

Sequence: 1 MKLPVRLVLMFWIPASNSD.....PQSHVPYAFGGTQKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	100.0	132	6	ABG74246 Mouse ant
2	646	94.2	131	2	AAR52772 Murine KC
3	646	94.2	131	2	AAR52790 Murine KC
4	646	94.2	131	2	AAR70457 VL sequen
5	645	94.0	238	2	AAY17416 Mouse imm
6	644	93.9	131	6	ABP72116 Mouse FGF
7	644	93.9	131	7	ADD28184 Mouse lec
8	644	93.9	131	7	ADE36480 Mouse ant
9	644	93.9	131	7	ADL35318 Murine an
10	639	93.1	149	2	AAR03199 Anti-idi
11	639	93.1	149	2	AAY21545 Monoclon
12	638	93.0	132	8	ADH17810 Murine an
13	637	92.9	131	2	AAR31587 BR55-2 li
14	637	92.9	131	2	AAR32241 ChimERIC
15	637	92.9	131	7	AAY42958 Mouse 12B
16	637	92.9	131	7	AAY42968 ChimERIC
17	637	92.9	139	7	ABR82782 Hybridoma
18	637	92.9	139	7	ABR82892 Hybridoma
19	635	92.6	149	2	AAY49209 MAB 1A7 1
20	635	92.6	149	2	AAY28468 Light cha
21	635	92.6	149	6	ADA14768 Mouse ant
22	635	92.6	149	7	ADC35310 Monoclon
23	633	92.3	149	8	ADL27486 Amino aci
24	631	92.0	131	2	AAR32245 BR55-2 mu
25	631	92.0	238	2	AAW14937 Murine an

26	631	92.0	238	2	AAW14942	Aaw14942 3F4 Human
27	630	91.8	132	2	AAW60867	Aaw60867 Variable
28	630	91.8	132	3	AAAY80294	Aay80294 IgM chime
29	630	91.8	144	8	ADM33981	Adm33981 Anti-NOGO
30	630	91.8	238	2	AAW31752	Aaw31752 L chain s
31	630	91.8	238	2	AAW71889	Aaw71889 Anti-huma
32	630	91.8	238	3	AAAB12909	Aab12909 Anti-huma
33	627	91.4	144	8	ADM33982	Adm33982 Anti-NOGO
34	625	91.1	132	4	AAAG67666	Aag67666 Amino aci
35	625	91.1	132	6	ABR40285	AbR40285 Murine am
36	625	91.1	238	6	ABP58288	Abp58288 Humanised
37	624	91.0	131	2	AAR52822	Aar52822 Humanised
38	624	91.0	131	2	AAR70470	Aar70470 Humanised
39	624	91.0	131	5	ABG76933	Abg76933 Mouse 10D
40	624	91.0	131	8	ADR88418	Adr88418 Murine 10
41	623	90.8	140	2	AAW68492	Aaw68492 Variable
42	620	90.4	131	7	ADE36531	Ade36531 Anti-FGF-
43	617	89.9	131	3	AAAB23812	Aab23812 Plasmid p
44	617	89.9	131	4	AAAG67488	Aag67488 Amino aci
45	617	89.9	131	5	AAW47626	Aam47626 Murine MA

ALIGNMENTS

RESULT 1

ABG74246

ID ABG74246 standard; protein; 132 AA.

XX AC ABG74246;

XX DT 22-APR-2003 (first entry)

XX DE Mouse antibody 4D4 light chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;
immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
3E11; prostate-specific membrane antigen; zeta signalling chain;
CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
small cell lung cancer; light chain variable region; mouse.

XX OS Mus sp.

XX PN US2002132983-A1.

XX PD 19-SEP-2002.

XX PF 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PA 30-NOV-2000; 2000US-0250089P.

XX PI (JUNG/) JUNGHANS R P.

XX DR Junghans RP;

XX DR WPI; 2003-208946/20.

XX DR N-PSDB; ABX16572.

XX PT New chimeric molecule useful in treating patients with disorders, such as
melanoma, neuroendocrine disorders, prostate and small cell lung cancer
comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 15-16; 35pp; English.

XX CC The invention relates to a chimaeric molecule comprising the GD3
(ganglioside antigen) binding domain of antibody MB3.6, with any of 3
variable gene sequences, or the PSMA (prostate-specific membrane antigen)
binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
sequences, the zeta signalling chain of the T cell receptor and an
intervening CD8alpha hinge in which cysteine residues have been mutated.
The chimaeric molecules expressed in T cells or NK cells or other
effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 4D4 light chain variable region
 XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 686; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.5e-52;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSISCRSSQSIHVSNGDTYLEWY 60
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSISCRSSQSIHVSNGDTYLEWY 60
 QY 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPVY 120
 DB 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPVY 120
 QY 121 AFGGGTKLEIKR 132
 DB 121 AFGGGTKLEIKR 132

RESULT 2
 AAR52772
 ID AAR52772 standard; protein; 131 AA.
 AC AAR52772;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-JAN-1995 (first entry)
 XX
 DE Murine KC-4 immunoglobulin light chain variable region (deduced).
 XX
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human milk fat globule; human breast carcinoma;
 KW murine anti-human carcinoma monoclonal antibody KC-4.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 FT Protein 20..131
 FT Region /label= KC-4_mature_VL-chain
 FT Region 20..42
 FT Region /label= FR1
 FT Region 43..58
 FT Region /label= CDR1
 FT Region 59..73
 FT Region /label= FR2
 FT Region 74..80
 FT Region /label= CDR2
 FT Region 81..112
 FT Region /label= FR3
 FT Modified-site 98..100
 FT /note= "putative glycosylation site"
 FT Region 113..121
 FT Region /label= CDR3
 FT Region 122..131
 FT Region /label= FR4

XX WO9411508-A2.
 XX
 XX 26-MAY-1994.
 XX
 XX 15-NOV-1993; 93WO-US011316.
 XX
 XX 13-NOV-1992; 92US-00977706.
 PR 13-NOV-1992; 92US-00977707.
 PR 28-SEP-1993; 93US-00128015.

XX
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 XX
 DR WPI; 1994-183509/22.
 DR N-PSDB; AAQ62763.
 XX
 PT Chimeric human-murine polypeptide(s) specific for human mammary fat
 PT globule antigen - for imaging, diagnosing and treating neoplasia, with
 PT less undesirable immunogenic response.
 XX
 PS Example 27; Page 41; 54pp; English.
 XX
 CC An initial isolation of cDNAs coding for murine anti-human breast
 CC carcinoma MAb KC-4 was performed using PCR with commercially available
 CC primers (see AAQ62751-Q62758, available from NOVAGEN). Subsequent cloning
 CC using PCR primers JO20, JO21, JO22 and JO24 (see AAQ62759-Q62762)
 CC resulted in the isolation of the mouse Ig variable domains. The amplified
 CC cDNAs were sequenced (AAQ62763 and AAQ62764) and amino acid sequences
 CC were deduced from them. Chimeric mouse-human antibodies were constructed
 CC using human constant regions so as to produce less immunogenic
 CC polypeptides which retained the anti-human carcinoma binding specificity
 CC of KC-4. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 131 AA;

Query Match 94.2%; Score 646; DB 2; Length 131;
 Best Local Similarity 93.9%; Pred. No. 4.9e-49;
 Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSISCRSSQSIHVSNGDTYLEWY 60
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSISCRSSQSIHVSNGDTYLEWY 60
 QY 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPVY 120
 DB 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPVY 120
 QY 121 AFGGGTKLEIKR 131
 DB 121 TFGGGTKLEIKR 131

RESULT 3
 AAR52790
 ID AAR52790 standard; protein; 131 AA.
 AC AAR52790;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-JAN-1995 (first entry)
 XX
 DE Murine KC-4 immunoglobulin light chain variable region (deduced).
 XX
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human milk fat globule; human breast carcinoma;
 KW murine anti-human carcinoma monoclonal antibody KC-4.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 FT Protein 20..131
 FT Region /label= KC-4_mature_VL-chain
 FT Region 20..42
 FT Region /label= FR1
 FT Region 43..58
 FT Region /label= CDR1
 FT Region 59..73
 FT Region /label= FR2
 FT Region 74..80
 FT Region /label= CDR2
 FT Region 81..112
 FT Region /label= FR3
 FT Modified-site 98..100

FT Region /note= "putative glycosylation site"
 FT 113. .121
 FT /label= CDR3
 FT 122. .131
 FT /label= FR4
 PN WO9411509-A2.
 XX 26-MAY-1994.
 XX 16-NOV-1993; 93WO-US011445.
 XX 16-NOV-1992; 92US-00977696.
 PR 30-SEP-1993; 93US-00129930.
 PR 08-OCT-1993; 93US-00134346.
 XX (CANC-) CANCER RES FUND CONTRA COSTA.
 XX Do Couto FJR, Ceriani RL, Peterson JA, Padlan EA;
 XX WPI; 1994-183510/22.
 XX New analogue peptide(s) comprising antibody variable regions - used to
 PT develop prods. for use in the detection, diagnosis, therapy and
 PT prevention of neoplasms.
 XX Example 26; Page 61; 109pp; English.
 XX An initial isolation of cDNAs coding for murine anti-human breast
 CC carcinoma MAB KC-4 was performed using PCR with commercially available
 CC primers (see AAQ62776-Q62783, available from NOVAGEN). Subsequent cloning
 CC using PCR primers JO20, JO21, JO22 and JO24 (see AAQ62784-Q62787)
 CC resulted in the isolation of the mouse Ig variable domains. The amplified
 CC cDNAs were sequenced (AAQ62788 and AAQ62789) and amino acid sequences
 CC were deduced from them. Chimeric mouse-human antibodies were constructed
 CC using human constant regions so as to produce less immunogenic
 CC polypeptides which retained the anti-human carcinoma binding specificity
 CC of KC-4. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 131 AA;
 SQ Query Match 94.2%; Score 646; DB 2; Length 131;
 Best Local Similarity 93.9%; Pred. No. 4.9e-49;
 Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MKLPVRLVLVFWIPASNSDVLMTQSLPLSVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Db 1 MKLPVRLVLVFWIPASSSDVLTQTPLSLPVLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Qy 61 LQKPGQSPKLLIYKVSIRFSGVPDRFSGSGSGTDFTLTKISRVEAEDLGVYFCFGSHVPY 120
 Db 61 LQKPGQSPKLLIYKVSIRFSGVPDRFSGSGSGTDFTLTKISRVEAEDLGVYFCFGSHVPY 120
 Qy 121 AFGGGTKLEIK 131
 Db 121 TFGGGTKLEIK 131
 RESULT 5
 AAY17416
 ID AAY17416 standard; protein; 238 AA.
 AC AAY17416;
 XX 26-JUL-1999 (first entry)
 DT Mouse immunoglobulin E light chain.
 DE Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
 KW Mus sp.
 XX Key 1. .19
 XX Location/Qualifiers
 FH Peptide /label= signal
 FT Protein 20. .238
 FT /label= immunoglobulin_E_light_chain
 XX

PN WO9510776-A1.
 XX 20-APR-1995.
 XX 16-NOV-1993; 93WO-US011444.
 XX 08-OCT-1993; 93US-00134346.
 XX (CANC-) CANCER RES FUND CONTRA COSTA.
 XX Do Couto JJR, Ceriani RL, Peterson JA;
 XX WPI; 1995-161912/21.
 DR N-PSDB; AAQ87531.
 XX New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of cancers.
 XX Example; Table 14, Page 31; 61pp; English.
 XX The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL were
 CC prepared by PCR from polyadenylated RNA isolated from 100 million KC-4
 CC hybridoma cells. All clones were obtd. from independent PCRs. The
 CC sequences of the primers are given in AAQ87519-Q87526. The PCR products
 CC were cloned, without prior purificn., into pCR1000 (Invitrogen) and
 CC sequenced in both directions. The VL DNA sequence and its derived protein
 CC sequences are shown in AAQ87531 and AAQ87531. The mature VL chain
 CC begins at AA D of framework 1 (FR1). VL is a group II kappa chain. Part
 CC of the CDR3 and all of the FR4 are encoded by Jk2. There is an
 CC asparagine glycosylation site in the light chain in FR3. The site reads
 CC NIS. AAQ870457 is a composite sequence of AAQ870449-R70456. (Updated on 25-
 CC MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 131 AA;
 SQ Query Match 94.2%; Score 646; DB 2; Length 131;
 Best Local Similarity 93.9%; Pred. No. 4.9e-49;
 Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MKLPVRLVLVFWIPASNSDVLMTQSLPLSVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Db 1 MKLPVRLVLVFWIPASSSDVLTQTPLSLPVLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Qy 61 LQKPGQSPKLLIYKVSIRFSGVPDRFSGSGSGTDFTLTKISRVEAEDLGVYFCFGSHVPY 120
 Db 61 LQKPGQSPKLLIYKVSIRFSGVPDRFSGSGSGTDFTLTKISRVEAEDLGVYFCFGSHVPY 120
 Qy 121 AFGGGTKLEIK 131
 Db 121 TFGGGTKLEIK 131
 RESULT 5
 AAY17416
 ID AAY17416 standard; protein; 238 AA.
 AC AAY17416;
 XX 26-JUL-1999 (first entry)
 DT Mouse immunoglobulin E light chain.
 DE Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
 KW Mus sp.
 XX Key 1. .19
 XX Location/Qualifiers
 FH Peptide /label= signal
 FT Protein 20. .238
 FT /label= immunoglobulin_E_light_chain
 XX

PN EP921189-A1.
 XX 09-JUN-1999.
 XX 13-NOV-1998; 98EP-00309340.
 XX 14-NOV-1997; 97JP-00313989.
 XX (SANY) SANKYO CO LTD.
 PA (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
 XX Karasuyama H, Yonemawa H, Taya C, Matsuoka K;
 PI WPI; 1999-315404/27.
 DR N-PSDB; AAX61085.
 XX Transgenic non-human animal allergy models.
 PT Claim 28; Page 30-32; 42pp; English.
 XX The present invention describes a transgenic, non-human animal with its
 CC genome altered to constitutively express a molecule having a constant
 CC region which can bind an IGE receptor on mast cells in the animals, the
 CC molecule having an immunoglobulin structure and being further capable of
 CC specifically binding a predetermined antigen. The transgenic animal is
 CC useful as a model for evaluating the activity and the ability of
 CC substances i.e. with anti-allergic activity, to affect any allergic
 CC reaction caused in the animal by the administration of the antigen to the
 CC animal, and applying the substance to be evaluated. The present sequence
 CC is the mouse immunoglobulin E (IgE) light chain, given in the present
 CC invention
 XX
 SQ Sequence 238 AA;
 Query Match 94.0%; Score 645; DB 2; Length 238;
 Best Local Similarity 93.2%; Pred. No. 1.1e-48;
 Matches 123; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTVLEWY 60
 DB 1 MKLPVRLVLMFWIPASSDVLMTQTPSLPVSLSGDAQSICRSSQSIHVSNGNTVLEWY 60
 QY 61 LQKPGQSPKLLIYKVDNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120
 DB 61 LQKPGQSPKLLIYKVNRRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPL 120
 QY 121 AFGGGTKLEIKR 132
 DB 121 TFGAGTKLEIKR 132
 RESULT 6
 ABP72116
 ID ABP72116 standard; protein; 131 AA.
 XX
 AC ABP72116;
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE Mouse FGF-8 related protein SEQ ID 4.
 XX
 KW Mouse; humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic;
 KW cancer; prostate; breast; ovarian; testicular.
 XX
 OS Mus musculus.
 XX WO2003002608-A1.
 PN
 XX 09-JAN-2003.
 XX 28-JUN-2002; 2002WO-JP006591.
 XX 28-JUN-2001; 2001JP-00196176.

XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Shitara K, Nakamura K, Hirota M, Shimada N;
 PI WPI; 2003-239169/23.
 DR N-PSDB; AB299466.
 XX Humanised antibodies and antibody fragments reacting with fibroblast
 PT growth factor 8 useful for the treatment and diagnosis of cancer.
 XX Example 1; Page 67-68; 86pp; Japanese.
 XX The invention relates to novel humanised antibodies and antibody
 CC fragments which react with fibroblast growth factor 8 (FGF8) and inhibit
 CC its biological functions. The polypeptides of the invention have
 CC cytostatic activity. The antibody is useful for the treatment of cancer,
 CC including prostate, breast, ovarian and testicular cancer. The present
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 131 AA;
 Query Match 93.9%; Score 644; DB 6; Length 131;
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTVLEWY 60
 DB 1 MKLPVRLVLMFWIPASSDVLMTQTPSLPVSLSGDAQSICRSSQSLVHSGRTVLEWY 60
 QY 61 LQKPGQSPKLLIYKVDNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120
 DB 61 LQKPGQSPKLLIYKVNRRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120
 QY 121 AFGGGTKLEIK 131
 DB 121 TFGGGTKLEIK 131
 RESULT 7
 ADD28184
 ID ADD28184 standard; protein; 131 AA.
 XX
 AC ADD28184;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Mouse lectin tolerance related protein SEQ ID NO:17.
 XX
 KW mouse; antibody; lectin; sugar; N-acetylglucosamine;
 KW FC gamma receptor IIIfa; cytostatic; anti-allergic; immunomodulator;
 KW cardiant; virucide; antibacterial; tumour; allergy; inflammation;
 KW autoimmune disease; circulatory system; viral infection;
 KW bacterial infection.
 XX
 OS Mus musculus.
 XX WO2003084570-A1.
 PN
 XX 16-OCT-2003.
 XX 09-APR-2003; 2003WO-JP004505.
 XX 09-APR-2002; 2002JP-00106951.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Nakamura K, Shitara K, Hatanaka S, Niwa R, Okazaki A;
 PI WPI; 2003-812677/76.
 DR N-PSDB; ADD28183.
 XX
 PT Drugs containing antibody compositions produced by cells tolerant to

PT lectin recognizing specific sugar-chain structure, appropriate for
 PT patients suffering from FcgammaRIIIa polymorphism e.g. in treating
 XX tumors.
 PS Example 3; SEQ ID NO 17; 214pp; Japanese.
 XX
 CC The invention relates to a novel drug containing as the active ingredient
 CC an antibody composition produced by cells tolerant to a lectin
 CC recognising a sugar-chain structure in which an alpha-bond is formed
 CC between the 6-position of N-acetylglucosamine at the reducing end of an N
 CC -glycoside bond-type complex sugar chain and the 1-position of fucose,
 CC which has affinity to human Fc gamma receptor IIIa. A drug of the
 CC invention has cytostatic, antiallergic, immunomodulator, cardiant,
 CC virucide, and antibacterial activity. The drugs are useful in screening
 CC and treating patients not suitable for drugs not derived from these
 CC cells, particularly as diagnostics, preventives or remedies for diseases
 CC accompanying tumour, allergy or inflammation, autoimmune diseases,
 CC diseases of the circulatory system, and viral or bacterial infections.
 CC The present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 131 AA;
 Query Match 93.9%; Score 644; DB 7; Length 131;
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MKLPVRLVLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MKLPVRLVLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60
 Qy 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
 Qy 121 AFGGGTKLEIK 131
 |||||:|||||
 Db 121 TFGGGTKLEIK 131
 |||||:|||||
 RESULT 8
 ADE36480
 ID ADE36480 standard; protein; 131 AA.
 AC ADE36480;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE Mouse anti-FGF-8 antibody-related protein #2.
 XX
 KW arthritis; anti-FGF-8; sic fibroblast growth factor;
 KW cartilage protection agent; joint destruction inhibitor;
 KW synovial proliferation inhibitor; mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN WO2003057251-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 26-DEC-2002; 2002WO-JP013650.
 XX
 PR 28-DEC-2001; 2001JP-00400677.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Tamura T, Uchii M, Suda T, Miki I, Tanaka A;
 XX
 DR WPI; 2003-587078/55.
 DR N-PSDB; ADE36479.
 XX
 XX Treatment and prevention of arthritis comprising the use of anti-FGF-8
 PT (sic fibroblast growth factor) antibody.
 XX

PS Example; SEQ ID NO 4; 193pp; Japanese.
 XX
 CC The invention comprises a method for treating and preventing arthritis,
 CC the method involves the use of anti-FGF-8 (sic fibroblast growth factor)
 CC antibody. The antibody and method of the invention is useful for: the
 CC detection, treatment and prevention of arthritis; as a cartilage
 CC protection agent; as a joint destruction inhibitor; and as a synovial
 CC proliferation inhibitor. The present amino acid sequence represents a
 CC mouse protein that was used in an example of the invention.
 XX
 SQ Sequence 131 AA;
 Query Match 93.9%; Score 644; DB 7; Length 131;
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MKLPVRLVLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MKLPVRLVLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60
 Qy 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
 Qy 121 AFGGGTKLEIK 131
 |||||:|||||
 Db 121 TFGGGTKLEIK 131
 |||||:|||||
 RESULT 9
 ADL35318
 ID ADL35318 standard; protein; 131 AA.
 XX
 AC ADL35318;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Murine anti-Fcgamma receptor IIIa antibody-related protein - SEQ 75.
 XX
 KW antibody binding; Fcgamma receptor IIIa; Fc region sugar chain;
 KW cytostatic; antiallergic; antiinflammatory; immunosuppressive;
 KW vasotropic; virucide; cancer; allergy; inflammatory; autoimmune;
 KW circulatory; viral infection; murine; mouse.
 XX
 OS Mus musculus.
 XX
 PN WO2003085119-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 09-APR-2003; 2003WO-JP004504.
 XX
 PR 09-APR-2002; 2002JP-00106950.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakamura K, Shitara K;
 XX
 DR WPI; 2003-812729/76.
 DR P-PSDB; ADL35317.
 XX
 PT Method of enhancing the binding activity of antibody to Fc-gamma receptor
 PT IIIa for production of antibodies with high cytotoxicity as cancer,
 PT allergic, viral and other disease therapeutic agents.
 XX
 PS Example 14; SEQ ID NO 75; 296pp; Japanese.
 XX
 CC The invention relates to a novel method for enhancing the binding
 CC activity of an antibody to the Fcgamma receptor IIIa by increasing the
 CC proportion of N-glycoside bond type complex sugar chains attached to the
 CC Fc region of the antibody which do not have the 1-position of fucose
 CC bound to the 6-position of N-acetylglucosamine at the reducing end of the
 CC sugar chain. The method of the invention has cytostatic, antiallergic,

CC antiinflammatory, immunosuppressive, vasotropic and virucide applications
 CC and may be useful for generating antibodies to be used in the treatment,
 CC prevention and diagnosis of diseases including cancer, allergies,
 CC inflammatory disorders, autoimmune diseases, circulatory disorders and
 CC viral infections. The current sequence is that of an anti-Fcγ₃ receptor
 CC receptor IIIa antibody-related protein of the invention.
 XX
 SQ Sequence 131 AA;

Query Match 93.9%; Score 644; DB 7; Length 131;
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFIPASNSDVLMTQSLPVSIGDQASISCRSSQSI VHSNGDTVLEWY 60
 DB 1 MKLPVRLVLMFIPASNSDVLMTQSLPVSIGDQASISCRSSQSI VHSNGRTVLEWY 60
 QY 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGDTFTLKISRVEADLGVYFCQGSHPVY 120
 DB 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGDTFTLKISRVEADLGVYFCQGSHPVY 120
 QY 121 AFGGGTKLEIK 131
 DB 121 TFGGGTKLEIK 131

RESULT 10
 AAW03199
 ID AAW03199 standard; protein; 149 AA.
 XX
 AC AAW03199;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-FEB-1997 (first entry)
 XX
 DE Anti-idiotype monoclonal antibody 1A7 variable light chain.

XX Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine;
 KW treatment; palliative; detection; diagnosis; recombinant production;
 KW purification; probe; primer; assay; amplification; gene therapy.
 XX
 OS Mus musculus.

Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Region 20..42
 FT /note= "framework region 1"
 FT Region 43..58
 FT /note= "complementarity determining region 1"
 FT Region 59..73
 FT /note= "framework region 2"
 FT Region 74..80
 FT /note= "complementarity determining region 2"
 FT Region 81..112
 FT /note= "framework region 3"
 FT Region 113..121
 FT /note= "complementarity determining region 3"
 FT Region 122..131
 FT /note= "framework region 4"

XX WO9622373-A2.
 XX
 XX 25-JUL-1996.
 XX
 XX 17-JAN-1996; 96WO-US0000882.
 XX
 XX 17-JAN-1995; 95US-00372676.
 PR 16-JAN-1996; 96US-00591196.
 XX

PA (KENT) UNIV KENTUCKY.
 XX Chatterjee M, Chatterjee SK, Foon KA;
 XX WPI; 1996-354530/35.
 DR N-PSDB; AAT311332.
 XX

PT Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
 PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
 PT glioma.
 XX

Claim 8; Fig 1; 141pp; English.

XX The present sequence is that of the murine anti-idiotype monoclonal
 CC antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the
 CC anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2.
 CC As the glycosphingolipid GD2 is expressed at high density by human
 CC neuroectodermal tumours, e.g. malignant melanoma, neuroblastoma, glioma,
 CC soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its
 CC cDNA can be used in a vaccine to treat or palliate such diseases. They
 CC can also be used to reduce the risk of recurrence of a clinically
 CC detectable tumour, and detect an anti-GD2 Ab bound to a tumour cell. MAb
 CC 1A7 overcomes immune tolerance and induces an immune response against
 CC GD2, which comprises anti-GD2 Ab (humoral response) and GD2-specific
 CC cells (cellular response). It can be used to purify anti-1A7 (Ab3), anti-
 CC GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or anti-GD2 in a sample or
 CC measure the level of cellular anti-1A7 or anti-GD2 activity. The cDNA can
 CC be used in expression systems for 1A7 prodn., and in the prepn. of probes
 CC and primers to respectively assay for 1A7 cDNA, and amplify desired
 CC polynucleotides for use in gene therapy. (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX

SQ Sequence 149 AA;

Query Match 93.1%; Score 639; DB 2; Length 149;
 Best Local Similarity 92.4%; Pred. No. 2.3e-48;
 Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFIPASNSDVLMTQSLPVSIGDQASISCRSSQSI VHSNGDTVLEWY 60
 DB 1 MKLPVRLVLMFIPASNSDVLMTQSLPVSIGDQASISCRSSQSI VHSNGTILEWY 60
 QY 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGDTFTLKISRVEADLGVYFCQGSHPVY 120
 DB 61 LQKPGSPKLLIYKVSDFSGVDPDRFSGSGGDTFTLKISRVEADLGVYFCQGSHPVY 120
 QY 121 AFGGGTKLEIKR 132
 DB 121 TFGGGTKLEIKR 132

RESULT 11
 AAY21545
 ID AAY21545 standard; protein; 149 AA.
 XX
 AC AAY21545;
 XX
 DT 03-AUG-1999 (first entry)

XX Monoclonal antibody 1A7 light chain variable region.
 XX Psoriasis; immunological response; anti-idiotype antibody; glutamate;
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;
 KW monoclonal antibody; 1A7.

XX Unidentified.
 XX WO925380-A2.
 XX
 XX 27-MAY-1999.
 XX
 XX 17-NOV-1998; 98WO-US024607.
 XX


```

PR 17-NOV-1997; 97US-0065774P.
PR 16-NOV-1998; 98US-00192838.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Chatterjee M, Foon KA;
XX
XX WPI. 1999-347407/29.
XX
XX N-PSDB; AAX60629.
XX
XX Treatment of psoriasis comprises administration of antigen which
XX simulates the generation of anti-idiotypic antibodies.
XX
XX Disclosure; Fig 2; 48pp; English.
XX
XX The invention provides a method of treating of psoriasis by administering
XX an antigen which has similar immunogenic properties to an antigen
XX expressed on cells of psoriatic tissue so that an immunological response
XX is elicited in the individual. The antigen stimulates the generation of
XX anti-idiotypic antibodies that neutralize the aberrant immune response
XX causing the psoriasis. The method is used to treat psoriasis, especially
XX chronic plaque, psoriasis, plaque-type psoriasis or psoriatic
XX arthritis. The compositions allow the individual's own immune system to
XX act against psoriatic tissue. The present sequence represents the light
XX chain variable region of monoclonal antibody 1A7
XX
XX Sequence 149 AA;
SQ
    Query Match      93.1%; Score 639; DB 2; Length 149;
    Best Local Similarity 92.4%; Pred. No. 2.3e-48;
    Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLTQTPLSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDTFLKISRVEADLGVYFCQGSHPVY 120
DB 61 LQKPGQSPNLLIYFVSNRFGSGGSGTDTFLKISRVEADLGVYFCQGSHPVW 120
QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132
RESULT 12
ADH17810
ID ADH17810 standard; protein; 132 AA.
XX
XX AC ADH17810;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Murine antibody EM164 light chain leader and variable region protein.
XX
XX KW antibody EM164; insulin-like growth factor-I receptor; IGF-IR antagonist;
XX breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
XX prostate; lung; synovial carcinoma; pancreatic; murine; mouse;
XX light chain leader; variable region.
XX
XX OS Mus sp.
XX
XX PN WO2003106621-A2.
XX
XX PD 24-DEC-2003.
XX
XX PF 12-JUN-2003; 2003WO-US016211.
XX
XX PR 14-JUN-2002; 2002US-00170390.
XX
XX PA (IMMU-) IMMUNOGEN INC.
XX
XX PI Singh R, Tavares DJ, Dagdigian NE;

```

```

XX WPI. 2004-082172/08.
XX
XX N-PSDB; ADH17809.
XX
XX Novel murine antibody EM164 or antibody fragment that specifically binds
XX to insulin-like growth factor-I-receptor useful for treating breast
XX cancer, colon cancer, lung cancer, prostate cancer.
XX
XX Example 1; SEQ ID NO 50; 155pp; English.
XX
XX The invention relates to a novel murine antibody EM164 or antibody
XX fragment that specifically binds to insulin-like growth factor-I receptor
XX (IGF-IR) where the antibody is an antagonist of the receptor, is
XX substantially devoid of agonist activity toward the receptor and is
XX capable of inhibiting the growth of a cancer cell by greater than 80% in
XX the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
XX The antibody of the invention may be useful for diagnosing or treating a
XX patient having a cancer selected from breast cancer, colon cancer,
XX ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
XX cancer, synovial carcinoma and pancreatic cancer. The current sequence is
XX that of the murine anti-IGF-IR antibody EM164-related protein of the
XX invention.
XX
XX Sequence 132 AA;
SQ
    Query Match      93.0%; Score 638; DB 8; Length 132;
    Best Local Similarity 92.4%; Pred. No. 2.5e-48;
    Matches 122; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLTQTPLSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDTFLKISRVEADLGVYFCQGSHPVY 120
DB 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDTFLKISRVEADLGVYFCQGSHPVP 120
QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132
RESULT 13
AAR31587
ID AAR31587 standard; protein; 131 AA.
XX
XX AC AAR31587;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 09-JUN-1993 (first entry)
XX
XX DE BR55-2 light chain variable domain.
XX
XX KW Monoclonal; antibody; MAb; light; heavy; chain; variable; region;
XX human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
XX expression vector; IgG1; IgG3; pVκ; pVg; pVg3; gamma; kappa; constant;
XX pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
XX antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis; cancer;
XX epithelial; breast; colorectal; ovarian; prostate; pancreatic; gastric;
XX small cell lung; immunotherapy; HIV.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX
XX FT Peptide 20..131
XX
XX FT /note= "Mature peptide"
XX
XX PN EP528767-A1.
XX
XX PD 24-FEB-1993.
XX
XX PF 18-AUG-1992; 92EP-00810633.
XX
XX

```

PR 21-AUG-1991; 91GB-00018013.
 XX 02-MAR-1992; 92GB-00004514.
 PA (SANO) SANDOZ LTD.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 XX Co MS, Loibner H;
 XX
 DR WPI; 1993-060580/08.
 DR N-PSDB; AAQ36536.
 XX
 PT Human-mouse chimeric monoclonal antibodies - recognise difucosyl Lewis
 PT blood group antigens Y-6 and B-7-2, useful for treating cancer and HIV
 PT infection.
 PT
 XX
 XX Disclosure; Fig 8; 65pp; English.
 XX
 CC The sequences given in AAR31587-88 represent the light and heavy chain
 CC variable regions respectively from the murine monoclonal (MAB) BR55-2.
 CC BR55-2 was used as a basis for the construction of a chimeric MAB which
 CC recognises the difucosyl Lewis blood group. Separate expression vectors
 CC were used to express the chimeric human BR55-2 IgG1 and IgG3 antibody
 CC light and heavy chains: pVg for the light chain, pVg for the gamma 1
 CC heavy chain and pVg3 for the gamma 3 heavy chain. The actual expressed
 CC chimeric BR55-2 light chain gene and the heavy chain gene consist of two
 CC adjacent parts. The kappa/gamma constant regions were built into the
 CC vectors pVg and pVg3c (or pVg3c) respectively and the variable regions
 CC were constructed by PCR. The resulting plasmids were used to transfect
 CC the host cell line sp2/O-Ag 14 by electroporation. The resulting MABs
 CC recognise the difucosyl Lewis blood group antigens Y-6 and B-7-2 but do
 CC not induce human anti-mouse antibody response. The MABs show a restricted
 CC binding specificity which is associated with a lack of cross-reactivity to
 CC related antigens expressed on blood cells eg. erythrocytes. This allows
 CC the MABs to be particularly useful for therapeutic use in humans. The
 CC MABs are useful in the diagnosis and treatment of cancer of epithelial
 CC origin, eg. breast, colorectal, ovarian, prostate, pancreatic or gastric
 CC cancer and small cell lung cancer. The MABs are also useful for
 CC immunotherapy of HIV infections since the Lewis Y antigen is also
 CC selectively expressed on HIV infected cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 131 AA;

Query Match 92.9%; Score 637; DB 2; Length 131;
 Best Local Similarity 93.1%; Pred. No. 3.1e-48;
 Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLLVFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHVSNGDTYLEWY 60
 DB 1 MKLPVRLVLLVFWIPASSDVLMTQSLPVSIGDQASISCRSSQSIHVSNGNTYLEWY 60
 QY 61 LQPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLTLSRVEAEDLGVYFCFGSHVPY 120
 DB 61 LQPGQSPKLLISKVNRFSGVDPDRFSGSGGTFTLTLSRVEAEDLGVYFCFGSHVPF 120
 QY 121 AFGGCTKLEIK 131
 DB 121 TFGSGTKLEIK 131

RESULT 14
 AAR32241
 ID AAR32241 standard; protein; 131 AA.
 XX
 AC AAR32241;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JUN-1993 (first entry)
 XX
 XX Chimeric MAB light chain variable region.
 DE Monoclonal; antibody; MAB; light; heavy; chain; variable; region;
 XX
 KW

KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
 KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;
 KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
 KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis; cancer;
 KW epithelial; breast; colorectal; ovarian; prostate; pancreatic; gastric;
 KW small cell lung; immunotherapy; HIV.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 PH Region 43..58
 FT /label= CDR1
 FT /note= "Claim 4"
 FT Region 74..80
 FT /label= CDR2
 FT /note= "Claim 4"
 FT Region 113..121
 FT /label= CDR3
 FT /note= "Claim 4"
 XX
 XX EP528767-A1.
 XX
 XX 24-FEB-1993.
 XX
 XX 18-AUG-1992; 92EP-00810633.
 XX
 XX 21-AUG-1991; 91GB-00018013.
 XX 02-MAR-1992; 92GB-00004514.
 XX
 XX (SANO) SANDOZ LTD.
 XX (SANO) SANDOZ PATENT GMBH.
 XX (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 XX Co MS, Loibner H;
 XX
 XX WPI; 1993-060580/08.
 XX N-PSDB; AAQ36529.
 DR
 DR Human-mouse chimeric monoclonal antibodies - recognise difucosyl Lewis
 PT blood group antigens Y-6 and B-7-2, useful for treating cancer and HIV
 PT infection.
 PT
 XX
 XX Claim 3; Page 18; 65pp; English.
 XX
 CC The sequences given in AAR32241-42 are the light and heavy chain variable
 CC regions respectively from a human/mouse chimeric monoclonal antibody
 CC (MAB) which recognises the difucosyl Lewis blood group. The murine MAB
 CC BR55-2 was used as a basis for the construction of this chimeric MAB.
 CC Separate expression vectors were used to express the chimeric human BR55-
 CC 2 IgG1 and IgG3 antibody light and heavy chains: pVg for the light chain,
 CC pVg for the gamma 1 heavy chain and pVg3 for the gamma 3 heavy chain. The
 CC actual expressed chimeric BR55-2 light chain gene and the heavy chain
 CC gene consist of two adjacent parts. The kappa/gamma constant regions were
 CC built into the vectors pVg and pVg1c (or pVg3c) respectively and the
 CC variable regions were constructed by PCR (see also AAQ36531-33). The
 CC resulting plasmids were used to transfect the host cell line sp2/O-Ag 14
 CC by electroporation. The resulting MABs recognise the difucosyl Lewis
 CC blood group antigens Y-6 and B-7-2 but do not induce human anti-mouse
 CC antibody response. The MABs show a restricted binding specificity which is
 CC associated with a lack of cross-reactivity to related antigens expressed
 CC on blood cells eg. erythrocytes. This allows the MABs to be particularly
 CC useful for therapeutic use in humans. The MABs are useful in the
 CC diagnosis and treatment of cancer of epithelial origin, eg. breast,
 CC colorectal, ovarian, prostate, pancreatic or gastric cancer and small
 CC cell lung cancer. The MABs are also useful for immunotherapy of HIV
 CC infections since the Lewis Y antigen is also selectively expressed on HIV
 CC infected cells. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 131 AA;
 SQ

Query Match 92.9%; Score 637; DB 2; Length 131;
 Best Local Similarity 93.1%; Pred. No. 3.1e-48;
 Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-15
Perfect score: 686
Sequence: 1 MKLPVRLVLMFWIPASNSD.....FQGSHPVYAFGGTKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	94.0	238	3	US-09-192-545-4
2	639	93.1	149	3	US-09-192-838B-2
3	639	93.1	149	3	US-09-324-191-2
4	637	92.9	131	1	US-08-053-171-5
5	637	92.9	131	1	US-08-053-171-9
6	635	92.6	149	2	US-08-752-844-2
7	635	92.6	149	2	US-08-591-196-2
8	635	92.6	149	4	US-09-293-533-2
9	624	91.0	131	1	US-08-129-930B-95
10	624	91.0	131	3	US-08-134-346A-50
11	624	91.0	131	3	US-08-976-288A-95
12	612	89.2	131	3	US-08-589-939-7
13	610	88.9	173	5	PCT-US91-02942-3
14	610	88.9	173	5	PCT-US91-02946-3
15	595	86.7	131	1	US-07-977-696C-11
16	595	86.7	131	1	US-08-129-930B-11
17	595	86.7	131	3	US-08-976-288A-11
18	580.5	84.6	127	1	US-08-482-882-45
19	580.5	84.6	127	2	US-08-483-389-45
20	580.5	84.6	127	2	US-08-487-113D-45
21	580.5	84.6	127	2	US-08-473-503-45
22	580.5	84.6	127	2	US-08-483-932-45
23	580.5	84.6	127	2	US-08-720-420A-45
24	580.5	84.6	127	3	US-08-714-017-45
25	580.5	84.6	127	3	US-08-475-680-45
26	562	81.9	249	4	US-08-726-219A-190
27	556	81.0	125	1	US-08-331-398A-67

28	556	81.0	125	2	US-08-331-397B-67	Sequence 67, Appl
29	556	81.0	125	2	US-08-759-804A-66	Sequence 66, Appl
30	555	80.9	247	3	US-09-227-693-34	Sequence 34, Appl
31	555	80.9	248	1	US-08-331-398A-34	Sequence 34, Appl
32	555	80.9	248	2	US-08-331-397B-34	Sequence 34, Appl
33	555	80.9	248	2	US-08-759-804A-34	Sequence 34, Appl
34	551	80.3	112	1	US-08-331-398A-48	Sequence 48, Appl
35	551	80.3	112	1	US-08-077-252B-3	Sequence 3, Appl
36	551	80.3	112	2	US-08-888-366-16	Sequence 16, Appl
37	551	80.3	112	2	US-08-331-397B-48	Sequence 48, Appl
38	551	80.3	112	2	US-08-759-804A-48	Sequence 48, Appl
39	551	80.3	112	3	US-09-002-753A-3	Sequence 3, Appl
40	551	80.3	112	3	US-09-227-693-48	Sequence 48, Appl
41	551	80.3	112	4	US-09-657-274-3	Sequence 3, Appl
42	551	80.3	112	5	PCT-US94-06687-3	Sequence 66, Appl
43	550	80.2	263	2	US-08-752-844-66	Sequence 66, Appl
44	550	80.2	263	4	US-09-293-533-66	Sequence 19, Appl
45	549	80.0	112	2	US-08-859-649-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-192-545-4
; Sequence 4, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-4

Query Match 94.0%; Score 645; DB 3; Length 238;
Best Local Similarity 93.2%; Pred. No. 4e-56;
Matches 123; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPVLSLGDQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPVLSLGDQASISCRSSQSIHNSGDTYLEWY 60
QY 61 LQKFGQSPKLLIYKVYDRFSGVDPFRFGSGSGTFTLKISRVEADLGVYFCQGSHPVY 120
Db 61 LQKFGQSPKLLIYKVYDRFSGVDPFRFGSGSGTFTLKISRVEADLGVYFCQGSHPVY 120
QY 121 AFGGTKLEIKR 132
Db 121 TFGAGTKLEIKR 132

RESULT 2

US-09-192-838B-2
; Sequence 2, Application US/09192838B
; Patent No. 6355244
; GENERAL INFORMATION:
; APPLICANT: POON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000500

```
; CURRENT APPLICATION NUMBER: US/09/192,838B
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PR1
; ORGANISM: Mus Musculus
; ORGANISM: Mus Musculus
US-09-192-838B-2

Query Match          93.1%; Score 639; DB 3; Length 149;
Best Local Similarity 92.4%; Pred. No. 8.9e-56;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLMTQTPLSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
DB 61 LQPGQSPNLLIYFVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPW 120

QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132

RESULT 3
US-09-324-191-2
; Sequence 2, Application US/09324191
; Patent No. 6562798
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
; APPLICANT: CHATTERJEE, Malaya
; APPLICANT: FORT, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000540
; CURRENT APPLICATION NUMBER: US/09/324,191
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: 60/065,774
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PR1
; ORGANISM: Mus Musculus
US-09-324-191-2

Query Match          93.1%; Score 639; DB 4; Length 149;
Best Local Similarity 92.4%; Pred. No. 8.9e-56;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLMTQTPLSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
DB 61 LQPGQSPNLLIYFVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPW 120

QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132

RESULT 4
US-08-053-171-5
; Sequence 5, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew.
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
```

```
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-5

Query Match          92.9%; Score 637; DB 1; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.2e-55;
Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLMTQTPLSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
DB 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPW 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 5
US-08-053-171-9
; Sequence 9, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew.
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
```

```

; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-9

Query Match          92.9%; Score 637; DB 1; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.2e-55;
Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

Qy 121 AFGGSKLEIK 131
Db 121 TFGSGTKLEIK 131

```

```

RESULT 6
US-08-752-844-2
; Sequence 2, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Roon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-2

Query Match          92.6%; Score 635; DB 2; Length 149;
Best Local Similarity 91.7%; Pred. No. 2.2e-55;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

Qy 121 AFGGSKLEIK 132
Db 121 TFGGSKLEIK 132

RESULT 7
US-08-591-196-2
; Sequence 2, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Roon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-196-2

```

```

Query Match          92.6%; Score 635; DB 2; Length 149;
Best Local Similarity 91.7%; Pred. No. 2.2e-55;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

```

Db 61 LQKPGSPNLLIYFVSNRFGVDPDRFGSGGDTFTLKISRVEADLGVYFCQGSHPV 120

Qy 121 AFGGKLEIKR 132
Db 121 TFGGKLEIKR 132

RESULT 8

US-09-293-533-2
; Sequence 2, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foot, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-293-533-2

Query Match 92.6%; Score 635; DB 4; Length 149;
Best Local Similarity 91.7%; Pred. No. 2.2e-55;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHVSNGDTYLEWY 60
Qy 61 LQKPGSPKLLIYKVSDRFGVDPDRFGSGGDTFTLKISRVEADLGVYFCQGSHPV 120
Db 61 LQKPGSPNLLIYFVSNRFGVDPDRFGSGGDTFTLKISRVEADLGVYFCQGSHPV 120
Qy 121 AFGGKLEIKR 132
Db 121 TFGGKLEIKR 132

RESULT 9

US-08-129-930B-95

; Sequence 95, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-129-930B-95
Query Match 91.0%; Score 624; DB 1; Length 131;
Best Local Similarity 90.1%; Pred. No. 2.3e-54;
Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHVSNGDTYLEWY 60
Qy 61 LQKPGSPKLLIYKVSDRFGVDPDRFGSGGDTFTLKISRVEADLGVYFCQGSHPV 120
Db 61 LQKPGSPQLLIYKVSIRESGVDPDRFGSGGDTFTLKISRVEADLGVYFCQGSHPV 120
Qy 121 AFGGKLEIKR 131
Db 121 TFGGKLEIKR 131
RESULT 10
US-08-134-346A-50
; Sequence 50, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51


```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-134-346A-50
;
; Query Match 91.0%; Score 624; DB 3; Length 131;
; Best Local Similarity 90.1%; Pred. No. 2.3e-54;
; Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 MKPLVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGNTYLEWY 60
; DB 1 MKPLVRLVLMFWIPASSSDVLMTQPLSLPVTGPEPASISCRSSQSIHNSGNTYLEWY 60
;
; QY 61 LQKQSPQLLIYKVSIRFSGVDPDRFSGSGGTDTLTKISRVEADLVGYFCQSHVPY 120
; DB 61 LQKQSPQLLIYKVSIRFSGVDPDRFSGSGGTDTLTKISRVEADLVGYFCQSHVPY 120
;
; QY 121 AFGGKTKLEIK 131
; DB 121 TFGGKTKLEIK 131
;
; RESULT 11
; US-08-976-288A-95
; Sequence 95, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: Go Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-134-346A-50
;
; Query Match 91.0%; Score 624; DB 3; Length 131;
; Best Local Similarity 90.1%; Pred. No. 2.3e-54;
; Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 MKPLVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGNTYLEWY 60
; DB 1 MKPLVRLVLMFWIPASSSDVLMTQPLSLPVTGPEPASISCRSSQSIHNSGNTYLEWY 60
;
; QY 61 LQKQSPQLLIYKVSIRFSGVDPDRFSGSGGTDTLTKISRVEADLVGYFCQSHVPY 120
; DB 61 LQKQSPQLLIYKVSIRFSGVDPDRFSGSGGTDTLTKISRVEADLVGYFCQSHVPY 120
;
; QY 121 AFGGKTKLEIK 131
; DB 121 TFGGKTKLEIK 131
;
; RESULT 12
; US-08-589-939-7
; Sequence 7, Application US/08589939
; Patent No. 6015662
; GENERAL INFORMATION:
; APPLICANT: Hackett, Jr., John R.
; APPLICANT: Hoff, Jane A.
; APPLICANT: Ostrow, David H.
; APPLICANT: Golden, Alan M.
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
; TITLE OF INVENTION: CONTROLS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,939
; FILING DATE:
; CLASSIFICATION: 424
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-589-939-7

Query Match      89.2%; Score 612; DB 3; Length 131;
Best Local Similarity 89.3%; Pred. No. 3.6e-53;
Matches 117; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVMTQSLPLVSLVPGDAQASISCRSSQSLVHSYNGTYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPW 120
QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 13
PCT-US91-02942-3
; Sequence 3, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ADHAW, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02946-3

Query Match      88.9%; Score 610; DB 5; Length 173;
Best Local Similarity 88.6%; Pred. No. 7.9e-53;
Matches 117; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPDSSDDVMTQSLPLVSLGDAQASISCRSSQSLVHSNGNYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPL 120
QY 121 AFGGGTKLEIKR 132
Db 121 TFGGGTKLEIKR 132
```

```
; MOLECULE TYPE: protein
PCT-US91-02942-3

Query Match      88.9%; Score 610; DB 5; Length 173;
Best Local Similarity 88.6%; Pred. No. 7.9e-53;
Matches 117; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPDSSDDVMTQSLPLVSLGDAQASISCRSSQSLVHSNGNYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPL 120
QY 121 AFGGGTKLEIKR 132
Db 121 TFGGGTKLEIKR 132

RESULT 14
PCT-US91-02946-3
; Sequence 3, Application PC/TUS9102946
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ROBINSON, MARTYN K
; APPLICANT: BRIGHT, SUSAN M
; TITLE OF INVENTION: HUMANIZED CHIMERIC ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02946
; FILING DATE: 19910429
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0576600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02946-3

Query Match      88.9%; Score 610; DB 5; Length 173;
Best Local Similarity 88.6%; Pred. No. 7.9e-53;
Matches 117; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPDSSDDVMTQSLPLVSLGDAQASISCRSSQSLVHSNGNYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPL 120
```

Qy 121 AFGGKLEIKR 132
Db 121 TFGGKLEIKR 132

RESULT 15
US-07-977-696C-11
; Sequence 11, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Fadlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-11

Query Match 86.7%; Score 595; DB 1; Length 131;
Best Local Similarity 86.3%; Pred No. 1.7e-51;
Matches 113; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLGSDQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASISDVMTQTLPLVSLGSDQASISCRSSQNLVHNGNTLYWY 60
Qy 61 LQKQSQSKLLIYKVSDRFGSGGSGTDTTLKISRVEADLGVYFCQGSHPY 120
Db 61 LQKQSQSKLLIYRASIRFGSGGSGTDTTLKISRVEADLGVYFCQGTHVPW 120
Qy 121 AFGGKLEIK 131
Db 121 TFGGKLEIK 131

Search completed: May 25, 2005, 15:58:26
Job time : 17.454 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773A-15
Perfect score: 686
Sequence: 1 MKLPVRLVLMFWIPASNSD.....FQGSHPVAFGGGKLEIKR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	100.0	132	13	US-10-006-773-15
2	644	93.9	131	15	US-10-434-469-6
3	644	93.9	131	17	US-10-409-608A-17
4	639	93.1	149	9	US-09-990-205-2
5	637	92.9	131	15	US-10-388-214A-2
6	637	92.9	139	15	US-10-372-481-29
7	637	92.9	139	15	US-10-371-797-29
8	635	92.6	149	14	US-10-153-401-2
9	633	92.3	149	15	US-10-226-795-27
10	625	91.1	132	9	US-09-796-744-16
11	625	91.1	132	14	US-10-231-452-64
12	624	91.0	131	10	US-09-947-839-95
13	624	91.0	131	14	US-10-010-942B-14

14	624	91.0	131	15	US-10-388-389-14	Sequence 14, Appl
15	624	91.0	131	16	US-10-703-713-14	Sequence 14, Appl
16	624	91.0	131	16	US-10-704-070-14	Sequence 14, Appl
17	624	91.0	131	17	US-10-232-030-14	Sequence 14, Appl
18	619	90.2	140	9	US-09-341-894-4	Sequence 4, Appl
19	617	89.9	131	14	US-10-138-505-6	Sequence 6, Appl
20	617	89.9	131	15	US-10-227-864A-85	Sequence 85, Appl
21	617	89.9	131	15	US-10-221-131-90	Sequence 90, Appl
22	617	89.9	131	15	US-10-399-518-114	Sequence 114, Appl
23	615	89.7	256	15	US-10-257-864A-98	Sequence 98, Appl
24	615	89.7	256	15	US-10-221-131-103	Sequence 103, Appl
25	615	89.7	256	15	US-10-399-518-127	Sequence 127, Appl
26	614	89.5	131	14	US-10-138-505-10	Sequence 10, Appl
27	614	89.5	131	15	US-10-257-864A-87	Sequence 87, Appl
28	614	89.5	131	15	US-10-221-131-92	Sequence 92, Appl
29	614	89.5	131	15	US-10-399-518-116	Sequence 116, Appl
30	608	88.6	131	17	US-10-687-035-27	Sequence 27, Appl
31	595	86.7	131	10	US-09-947-839-11	Sequence 11, Appl
32	594	86.6	131	17	US-10-735-316A-63	Sequence 63, Appl
33	593	86.4	131	17	US-10-735-316A-67	Sequence 67, Appl
34	586	85.4	131	17	US-10-687-035-29	Sequence 29, Appl
35	584	85.1	122	17	US-10-735-316A-49	Sequence 49, Appl
36	580.5	84.6	127	9	US-09-753-436-45	Sequence 45, Appl
37	580.5	84.6	127	14	US-10-163-942-45	Sequence 45, Appl
38	562.5	82.0	132	15	US-10-388-214A-6	Sequence 6, Appl
39	562	81.9	249	16	US-10-803-622-190	Sequence 190, Appl
40	562	81.9	249	16	US-10-803-653-190	Sequence 190, Appl
41	559	81.5	112	10	US-09-995-529-10	Sequence 10, Appl
42	559	81.5	112	11	US-09-995-529-10	Sequence 10, Appl
43	559	81.5	112	17	US-10-735-316A-56	Sequence 56, Appl
44	556	81.0	112	17	US-10-735-316A-57	Sequence 57, Appl
45	553	80.6	112	15	US-10-434-469-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-10-006-773-15
; Sequence 15, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-15

Query Match 100.0%; Score 686; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 9.5e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPPLSLPVSLGDAQISCRSSQSIHNSGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASNSDVLMTQSPPLSLPVSLGDAQISCRSSQSIHNSGDTYLEWY 60
QY 61 LQKPEQSPKLLIYKVYSDRFGSGSGTFTLKISRVEADLGVYFCQGSHPY 120
DB 61 LQKPEQSPKLLIYKVYSDRFGSGSGTFTLKISRVEADLGVYFCQGSHPY 120
QY 121 AFGGKLEIKR 132
DB 121 AFGGKLEIKR 132


```

; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-214A-2

Query Match      92.9%; Score 637; DB 15; Length 131;
Best Local Similarity 92.4%; Pred. No. 3.8e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120

Qy 121 AFGGKTLEIKR 131
Db 121 TFGAGTKLEIKR 131

RESULT 6
US-10-372-481-29
; Sequence 29, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; TYPE: PRT
; LENGTH: 139
; ORGANISM: Homo sapiens
US-10-372-481-29

Query Match      92.9%; Score 637; DB 15; Length 139;
Best Local Similarity 91.7%; Pred. No. 4.1e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120

Qy 121 AFGGKTLEIKR 131
Db 121 TFGAGTKLEIKR 131

RESULT 7
US-10-371-797-29
; Sequence 29, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; ANTI-BODIES

```

```

; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 139
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-29

Query Match      92.9%; Score 637; DB 15; Length 139;
Best Local Similarity 91.7%; Pred. No. 4.1e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCFQSHVPY 120

Qy 121 AFGGKTLEIKR 132
Db 121 TFGGKTLEIKR 132

RESULT 8
US-10-153-401-2
; Sequence 2, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Chatterjee, Sunil K.
; Foon, Kenneth A.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792

```

```

;
; TELEX: 706141
;
; INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 149 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;
;     MOLECULE TYPE: protein
;
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-153-401-2

Query Match          92.6%;   Score 635;   DB 14;   Length 149;
Best Local Similarity 91.7%;   Pred. No. 6.8e-52;
Matches 121; Conservative    6; Mismatches    5; Indels    0; Gaps    0

QY      1  MKLPVRLILVLMFWIPASNDVLMTQSPULSPVSLGDAQASICRSSQSIVHSNGDITVLEWY 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  MKLPVRLILVLMFWIPASDDVFMQTQTPULSPVSLGDAQASICRSSQSIVHSNGNTVLEWY 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61  LQKPGQS PKLLIYKVYSDRFSFGSGSGTDTFTLKISRVEAEDLGVVYFCFGSHVPY 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  LQKPGQSNLLIYFYVSNRFSFGSGSGTDTFTLKISRVEAEDLGVVYFCFGSHVPM 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      121  AFGGKTQLEIKR 132
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      121  TFGGKTQLEIKR 132
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

APPLICANT: HANAI, NOBUO
APPLICANT: SHOJI, EMI
APPLICANT: SAKURADA, MIKKIKO
APPLICANT: FURUYA, AKIKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NIWA, RINPEI
APPLICANT: SHIBATA, KENJI
APPLICANT: YAMASAKI, MOTOO
TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-170
CURRENT APPLICATION NUMBER: US/09/796,744
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: JP 2000-59508
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 2000-401563
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 132
TYPE: PRT
ORGANISM: Mus musculus
US-09-796-744-16

US-09-798-744-18
; Sequence 16, Application US/09796744
; Patent No. US2002098527A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA

QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120
 Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120
 QY 121 AFGGGTKLEIKR 132
 Db 121 TFGGTRLEIKR 132

RESULT 12
 US-09-947-839-95
 ; Sequence 95, Application US/09947839
 ; Publication No. US20030138428A1
 ; GENERAL INFORMATION:
 ; APPLICANT: do Couto Dr., Fernando J.R.
 ; Ceriani Dr., Roberto L.
 ; Peterson Dr., Jerry A.
 ; Padlan Dr., Eduardo A.
 ; TITLE OF INVENTION: Analogue Peptides With Broad
 ; Carcinoma Specificity, and Kit and
 ; Diagnostic Vaccination and
 ; Therapeutic Methods
 ; NUMBER OF SEQUENCES: 95
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder & Poplawski
 ; STREET: 444 South Floor St., 19th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/09/947,839
 ; FILING DATE: 06-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/976,288
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 07/977,696
 ; FILING DATE: NO. US20030138428A1ember 16, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Viviana Amzel Ph.D.
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: P6639938
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 622-7700
 ; TELEFAX: (213) 489-4210
 ; TELEX: n.a.
 ; INFORMATION FOR SEQ ID NO: 95:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Query Match 91.0%; Score 624; DB 10; Length 131;
 Best Local Similarity 90.1%; Pred. No. 6.3e-51;
 Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120
 Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120

QY 121 AFGGGTKLEIK 131
 Db 121 TFGGGTKLEIK 131
 RESULT 13
 US-10-010-942B-14
 ; Sequence 14, Application US/10010942B
 ; Publication No. US20030165496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Gurig
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; FILE REFERENCE: ELN-002
 ; CURRENT APPLICATION NUMBER: US/10/010,942B
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: US 60/251,892
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1).....(19)
 ; US-10-010-942B-14

Query Match 91.0%; Score 624; DB 14; Length 131;
 Best Local Similarity 88.5%; Pred. No. 6.3e-51;
 Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60
 QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120
 Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSHVPY 120

QY 121 AFGGGTKLEIK 131
 Db 121 TFGAGTKLELE 131
 RESULT 14
 US-10-388-389-14
 ; Sequence 14, Application US/10388389
 ; Publication No. US2004008777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Gurig
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; FILE REFERENCE: ELN-002CP
 ; CURRENT APPLICATION NUMBER: US/10/388,389
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 10/010,942
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: US 60/251,892
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: SIGNAL

```
; LOCATION: (1)...(19)
US-10-388-389-14

Query Match          91.0%; Score 624; DB 15; Length 131;
Best Local Similarity 88.5%; Pred. No. 6.3e-51;
Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVLLVLMFWIPASNSDVLMTQSLPVSLSGDAQASISCRSSQSIHVSNGDTYLEWY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MKLPVLLVLMFWIPASSDVLMTQTPSLPVSLSGDAQASISCRSSQNIHVSNGNTYLEWY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPVY 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQKPGQSPKLLIYKVNRRFSGVDPDRFSGSGGTDTFTLKIKVVEAEDLGIYFCQGSHPV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 AFGGTYKLEIK 131
   |||||:
Db 121 TFGAGTKLELE 131
   |||||:
```

```
RESULT 15
US-10-703-713-14
; Sequence 14, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saidanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-14
```

```
Query Match          91.0%; Score 624; DB 16; Length 131;
Best Local Similarity 88.5%; Pred. No. 6.3e-51;
Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVLLVLMFWIPASNSDVLMTQSLPVSLSGDAQASISCRSSQSIHVSNGDTYLEWY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MKLPVLLVLMFWIPASSDVLMTQTPSLPVSLSGDAQASISCRSSQNIHVSNGNTYLEWY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPVY 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQKPGQSPKLLIYKVNRRFSGVDPDRFSGSGGTDTFTLKIKVVEAEDLGIYFCQGSHPV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 AFGGTYKLEIK 131
   |||||:
Db 121 TFGAGTKLELE 131
   |||||:
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773A-15
Perfect score: 686
Sequence: 1 MKLPVRLVLMFWIPASNSD.....FQGSHPVYAFGGTKLEIKR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	94.2	131	2 B39276	Ig light chain pre
2	627	91.4	131	2 B34904	Ig kappa chain pre
3	623	90.8	131	2 B32513	Ig kappa chain pre
4	623	90.8	131	2 C34904	Ig kappa chain pre
5	620	90.4	131	2 B30577	Ig kappa chain pre
6	619	90.2	131	2 D34904	Ig kappa chain pre
7	618	90.1	131	2 S09259	Ig kappa chain pre
8	616	89.8	132	2 PH0106	anti-digoxin trans
9	611	89.1	131	2 G34903	Ig kappa chain pre
10	601	87.6	131	2 S52449	Ig kappa chain v r
11	599.5	87.4	131	2 D29380	Ig kappa chain pre
12	594	86.6	131	2 PT0178	Ig kappa chain pre
13	593	86.4	119	2 A49032	Ig kappa chain v r
14	591.5	86.2	130	2 C29380	Ig kappa chain pre
15	590	86.0	118	2 S24503	Ig kappa chain v r
16	585	85.3	118	2 S24500	Ig kappa chain v r
17	584	85.1	118	2 S24529	Ig kappa chain v r
18	583	85.0	118	2 S24536	Ig kappa chain v r
19	581	84.7	118	2 S24535	Ig kappa chain v r
20	578	84.3	118	2 S24533	Ig kappa chain v r
21	571	83.2	118	2 S24532	Ig kappa chain v r
22	568	82.8	118	2 S24530	Ig kappa chain v r
23	567	82.7	118	2 S24538	Ig kappa chain v r
24	558	81.3	118	2 S24506	Ig kappa chain v r
25	558	81.3	118	2 S24509	Ig kappa chain v r
26	557	81.2	219	2 PC4203	Ig kappa chain (mo
27	556	81.0	112	2 A31807	Ig kappa chain v r
28	555	80.9	110	2 S26335	Ig kappa chain v r
29	554	80.8	219	2 S52028	Ig kappa chain - m

RESULT 1
B39276
Ig light chain precursor V-D-J region (6-19) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: B39276
R:Reininger, L.; Herney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A:Title: Cryoglobulinemia induced by a murine IGG3 rheumatoid factor: skin vasculitis ar
A:Reference number: A39276; MUID:91088540; PMID:2263605
A:Accession: B39276
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <REI>
A:Cross-references: GB:M55313; NID:g198095; PIDN:AAA63385.1; PID:g198096
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 94.2%; Score 646; DB 2; Length 131;
Best Local Similarity 93.9%; Pred. No. 1.3e-50;
Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVLSLGDQASISCRSSQSIHSHNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPVSSDVLMTQTPVLSLGDQASISCRSSQSIHSHNGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQGSHPVY 120
Db 61 LQKPGQSPKLLIYKVSRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQGSHPVY 120

Qy 121 AFGGGTKLEIK 131
Db 121 TFGSGTKLEIK 131

RESULT 2
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reac
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PID:g
C:Superfamily: immunoglobulin V region; immunoglobulin homology

ALIGNMENTS

C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 627; DB 2; Length 131;
Best Local Similarity 90.8%; Pred. No. 6.6e-49;
Matches 119; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSVLGDAQISCRSSQSIYHNSGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSLPSVLGDAQISCRSSQSLVHNSGNTYLVHWY 60

QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
DB 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 3
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: B32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: B32513
A;Molecule type: DNA
A;Residues: 1-131 <KOF>
A;Cross-references: GB:M20828; NID:gl96937; PIDN:AAA38843.1; PID:gl96938
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 623; DB 2; Length 131;
Best Local Similarity 90.8%; Pred. No. 1.5e-48;
Matches 119; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSVLGDAQISCRSSQSIYHNSGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSLPSVLGDAQISCRSSQSLVHNSGNTYLVHWY 60

QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
DB 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 4
C34904
Ig kappa chain precursor V region (3-24) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: C34904; I31485
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-re-
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 <BED>
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi

A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: I31485
A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-52 <BE2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 623; DB 2; Length 131;
Best Local Similarity 90.1%; Pred. No. 1.5e-48;
Matches 118; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSVLGDAQISCRSSQSIYHNSGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSLPSVLGDAQISCRSSQSLVHNSGNTYLVHWY 60

QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
DB 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 5
B30577
Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 09-Jul-2004
C;Accession: B30577
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theo
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rel
A;Reference number: A30577; MUID:85159423; PMID:3920343
A;Accession: B30577
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 <KOF>
A;Cross-references: UNIPROT:Q8VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.4%; Score 620; DB 2; Length 131;
Best Local Similarity 90.1%; Pred. No. 2.7e-48;
Matches 118; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSVLGDAQISCRSSQSIYHNSGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSLPSVLGDAQISCRSSQSLVHNSGNTYLVHWY 60

QY 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
DB 61 LQKPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 6
D34904
Ig kappa chain precursor V region (3-13) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C;Accession: D34904
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-re
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: D34904

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-131 <BED>

A;Cross-references: GB:L39105; NID:g639658; PIDN:AAA61590.1; PID:g639659

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 619; DB 2; Length 131;
Best Local Similarity 89.3%; Pred. No. 3.4e-48;
Matches 117; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60

Db 1 MKLPVRLVLMFWIPASSSDVVMVTQPLSLPVSLGDAQASISCRSSQSIHNSGNTYLRWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120

Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHTVPP 120

Qy 121 AFGGGTKLEIK 131

Db 121 TFGGGTKLEIK 131

RESULT 7

S09259

Ig kappa chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 21-Jan-2000

C;Accession: S09259

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRX

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09259

A;Molecule type: mRNA

A;Residues: 1-131 <HAM>

A;Cross-references: EMBL:X51720; NID:g53213; PIDN:CAA36013.1; PID:g53214

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 618; DB 2; Length 131;
Best Local Similarity 90.1%; Pred. No. 4.1e-48;
Matches 118; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60

Db 1 MKLPVRLVLMFWIPASSSDVVMVTQPLSLPVSLGDAQASISCRSSQSIHNSGNTYLRWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120

Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQASHPPR 120

Qy 121 AFGGGTKLEIK 131

Db 121 TFGGGTKLEIK 131

RESULT 8

PH0106

anti-digoxin transfectoma antibody heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: PH0106

R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.

Mol. Immunol. 27, 901-909, 1990

A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain

A;Reference number: PH0105; MUID:91015092; PMID:2120577

A;Accession: PH0106

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-132 <NEA>

A;Cross-references: UNIPROT:Q8VCI6

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 616; DB 2; Length 132;
Best Local Similarity 89.4%; Pred. No. 6.3e-48;
Matches 118; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60

Db 1 MKLPVRLVLMFWIPASSSDVVMVTQPLSLPVSLGDAQASISCRSSQSIHNSGNTYLRWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120

Db 61 LQKAGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGIYFCQSTHVP 120

Qy 121 AFGGGTKLEIKR 132

Db 121 TFGGGTKLEIKR 132

RESULT 9

G34903

Ig kappa chain precursor V region (10-25) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000

C;Accession: G34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reac

A;Reference number: A34903; MUID:90094387; PMID:2104617

A;Accession: G34903

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-131 <BED>

A;Cross-references: GB:M32381; GB:J05237; GB:J05238; NID:g639654; PIDN:AAA61588.1; PID:g

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 611; DB 2; Length 131;
Best Local Similarity 87.8%; Pred. No. 1.7e-47;
Matches 115; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60

Db 1 MKLPVRLVLMFWIPASSSDVVMVTQPLSLPVSLGDAQASISCRSSQSIHNSGNTYFFHWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120

Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQSTHVP 120

Qy 121 AFGGGTKLEIK 131

Db 121 TFGAGTKLEIK 131

RESULT 10

S52449

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: S52449

R;Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A;Description: Specific amplification by the polymerase chain reaction of rearranged ge

A;Reference number: S52445

A;Accession: S52449

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-131 <BER>

A;Cross-references: EMBL:X82691; NID:g673446; PIDN:CAAS8012.1; PID:g673447

C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 601; DB 2; Length 131;
Best Local Similarity 85.5%; Pred. No. 1.3e-46;
Matches 112; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASICRSSQSI VHSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPVSSDDVVMVTQTPSLPVLGDAQASICRSSQSLVHNGDTYLYHWY 60

QY 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 120
DB 61 LQKPGSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 11
D29380
IG kappa chain precursor V region (B003 46/2D7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: D29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: D29380
A;Molecule type: mRNA
A;Residues: 1-131 <CHE>
A;Cross-references: UNIPROT:Q8VC16
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 87.4%; Score 599.5; DB 2; Length 131;
Best Local Similarity 87.9%; Pred. No. 1.8e-46;
Matches 116; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASICRSSQSI VHSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVVMVTQTPSLPVLGDAQASICRSSQSLVHNGDTYLOWY 59

QY 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 120
DB 60 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 119

QY 121 AFGGGTKLEIK 132
DB 120 TFGGGTKLEIK 131

RESULT 12
PT0178
IG kappa chain precursor V region (IDB5.7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PT0178
R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A;Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid
A;Reference number: PT0174; MUID:91287738; PMID:1712074
A;Accession: PT0178
A;Molecule type: mRNA
A;Residues: 1-131 <PER>
A;Cross-references: UNIPROT:Q8VC16
A;Experimental source: strain BALB/c

C;Comment: IDB5.7 is an antibody to anti-alpha (1-6) dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 594; DB 2; Length 131;
Best Local Similarity 85.5%; Pred. No. 5.7e-46;
Matches 112; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASICRSSQSI VHSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVVMVTQTPSLPVLGDAQASICRSSQSLVHNGDTYLYHWY 60

QY 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 120
DB 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 120

QY 121 AFGGGTKLEIK 131
DB 121 TFGAGTKLEIK 131

RESULT 13
A49032
IG kappa chain V region (anti-phenylloxazalone) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Accession: A49032; S24528; S24512
R;Kaartinen, M.; Solin, M.L.; Makela, O.
Eur. J. Immunol. 21, 2863-2869, 1991
A;Title: V genes of oxazolone antibodies in 10 strains of mice.
A;Reference number: A49032; MUID:92037836; PMID:1936125
A;Accession: A49032
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <KAA>
A;Cross-references: GB:S64186; NID:G238586; PIDN:AAB20266.1; PID:G238587
A;Experimental source: C57BL/10
A;Note: sequence extracted from NCBI backbone (NCBIN:64186, NCBIP:64193)
R;Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24490
A;Accession: S24528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <XA2>
A;Cross-references: EMBL:X66624; EMBL:X66631
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 593; DB 2; Length 119;
Best Local Similarity 95.0%; Pred. No. 6.3e-46;
Matches 113; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASICRSSQSI VHSNGDTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVVMVTQTPSLPVLGDAQASICRSSQSI VHSNGDTYLEWY 60

QY 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 119
DB 61 LQKPGQSPKLLIYKVDPSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 119

RESULT 14
C29380
IG kappa chain precursor V region (BC-1004) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jul-2000
C;Accession: C29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable

A:Reference number: A92612; MUID:88007582; PMID:3115981
A:Accession: C29380
A:Molecule type: mRNA
A:Residues: 1-130 <CHE>
A:Cross-references: GB:M17162; GB:J02815; NID:g196899; PIDN:AAA38826.1; PID:g196900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 591.5; DB 2; Length 130;
Best Local Similarity 87.8%; Pred. No. 9.4e-46;
Matches 115; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

Qy 2 KLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHSHNGDITYLEWYL 61
Db 1 KLPVRLVLMFWIPASSDVLMTQSPLSPLVSLGDAQASISCRSSQSLVHSHNGNTYLQWYL 60

Qy 62 OKPGQSPKLLIYKVSDRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPYA 121
Db 61 OKPGQSPKLLIYTVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHTL-RT 119

Qy 122 FGGGTKLEIKR 132
Db 120 FGGGTKLEIKR 130

RESULT 15
S24503
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24503; S24499
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24503
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <KAA>
A:Cross-references: UNIPROT:Q99M37; EMBL:X66640; EMBL:X66636
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 590; DB 2; Length 118;
Best Local Similarity 95.8%; Pred. No. 1.1e-45;
Matches 113; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHSHNGDITYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQSPLSPLVSLGDAQASISCRSSQSLVHSHNGNTYLEWY 60

Qy 61 LOKPGQSPKLLIYKVSDRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHV 118
Db 61 LOKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHV 118

Search completed: May 25, 2005, 16:48:40
Job time : 18.6642 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.3423 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773a-15
Perfect score: 686
Sequence: 1 MKLPVRLVLMFWIPASNSD.....PQGSHPVYAFGGGTKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	80.9	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
2	524	76.4	113	1 KV2G MOUSE	P01631 mus musculus
3	518.5	75.6	239	2 Q8TCD0	Q8tcd0 homo sapien
4	514.5	75.0	133	1 KV2F HUMAN	P06310 homo sapien
5	505	73.6	219	2 Q65ZC0	Q65zc0 mus musculus
6	497.5	72.5	239	2 Q6P491	Q6p491 homo sapien
7	494.5	72.1	239	2 Q8NEK0	Q8nek0 homo sapien
8	480	70.0	240	2 Q6PIH6	Q6pih6 homo sapien
9	456	66.5	117	1 KV2E HUMAN	P06309 homo sapien
10	448	65.3	113	1 KV2D_HUMAN	P01617 homo sapien
11	447.5	65.2	114	2 Q9UL80	Q9ul80 homo sapien
12	445	64.9	113	1 KV2B HUMAN	P01615 homo sapien
13	434	63.3	113	1 KV2E MOUSE	P03976 mus musculus
14	431.5	62.9	115	1 KV2A_HUMAN	P01614 homo sapien
15	420.5	61.3	112	1 KV2C_HUMAN	P01616 homo sapien
16	415	60.5	112	1 KV2D_MOUSE	P01629 mus musculus
17	413	60.2	113	1 KV2F_MOUSE	P01630 mus musculus
18	401	58.5	134	1 KV4C HUMAN	P06314 homo sapien
19	400.5	58.4	133	1 KV4B HUMAN	P06313 homo sapien
20	396	57.7	112	2 Q6LEM8	Q6lem8 mus musculus
21	390.5	56.9	114	1 KV4A_HUMAN	P01625 homo sapien
22	388.5	56.6	132	1 KV3F_MOUSE	P01658 mus musculus
23	386.5	56.3	131	1 KV3I_MOUSE	P01661 mus musculus
24	383.5	55.9	235	2 Q6GMV9	Q6gmv9 homo sapien
25	382.5	55.8	129	1 KV3L HUMAN	P18135 homo sapien
26	381.5	55.6	129	1 KV3M_HUMAN	P18136 homo sapien
27	380.5	55.5	238	2 Q66J57	Q66j57 mus musculus
28	380	55.4	236	2 Q6PIL8	Q6pil8 homo sapien
29	379.5	55.3	108	1 KV1_CANFA	P01618 canis famil
30	378	55.1	113	1 KV2C_MOUSE	P01628 mus musculus
31	373	54.4	128	1 KV3K_HUMAN	P06311 homo sapien

32 372.5 54.3 120 1 KV2B_MOUSE P01627 mus musculus
33 370 53.9 236 2 Q6GMX8 Q6gmX8 homo sapien
34 369.5 53.9 255 2 Q6KB05 Q6kb05 mus musculus
35 369 53.8 236 2 Q6P5S8 Q6p5s8 homo sapien
36 368.5 53.7 111 1 KV3L_MOUSE P01664 mus musculus
37 368.5 53.7 235 2 Q6GMW0 Q6gmw0 homo sapien
38 366 53.4 112 1 KV2A_MOUSE P01626 mus musculus
39 365.5 53.3 111 1 KV3H_MOUSE P01660 mus musculus
40 365 53.2 236 2 Q6GMW1 Q6gmw1 homo sapien
41 364 53.1 236 2 Q7TS98 Q7ts98 mus musculus
42 362.5 52.8 111 1 KV3M_MOUSE P01665 mus musculus
43 361.5 52.7 111 1 KV3O_MOUSE P01667 mus musculus
44 361.5 52.7 111 2 Q920B9 Q920e9 mus musculus
45 361.5 52.7 129 1 KV3H_HUMAN P04207 homo sapien

ALIGNMENTS

RESULT 1

Q65ZQ7 PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57590; AAB19971.2; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 80.9%; Score 555; DB 2; Length 248;
Best Local Similarity 93.8%; Pred. No. 1.7e-48;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 19 SDVLTQSPSLPVSIGDQASISCRSSQSIIVHSNGDTYLEWYLPKPGQSPKLLIYKVDNR 78
|||||
Db 135 SDVLTQSPSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLPKPGQSPKLLIYKVNRR 194
|||||
Qy 79 FSGVDPFRFSGSGSGTDFTLKISRVEAEDLVYFCFQGSHPVYAFGGGTKLEIK 131
|||||
Db 195 FSGVDPFRFSGSGSGTDFTLKISRVEAEDLVYFCFQGSHPVYAFGGGTKLEIK 247
|||||

RESULT 2

KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83178921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 anti-digoxin hybridoma antibody";
 RL Biochemistry 22:1153-1158(1983).
 CC -I- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
 protein that binds digoxin.
 DR PIR; A01914; KVM26.
 DR HSP; Q99M37; 1191.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
 KW Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 39 Complementarity-determining-1.
 FT DOMAIN 40 54 Framework-2.
 FT DOMAIN 55 61 Complementarity-determining-2.
 FT DOMAIN 62 93 Framework-3.
 FT DOMAIN 94 102 Complementarity-determining-3.
 FT DOMAIN 103 112 Framework-4.
 FT DISULFID 23 93 By similarity.
 FT NON TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;
 Query Match 76.4%; Score 524; DB 1; Length 113;
 Best Local Similarity 88.5%; Pred. No. 9.6e-46;
 Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 20 DVLMTQPSLPSVSLGDSQASISCRSSQSIIVHNGDTYLEWYKQPCQSPKLIYKVSDFR 79
 DB 1 DVMTQTPSLPSVSLGDSQASISCRSSQSIIVHNGDTYLEWYKQPCQSPKLIYKVSDFR 60
 QY 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVYPYAFGGGTGLEIKR 132
 DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVYPYAFGGGTGLEIKR 113
 RESULT 3
 Q8TCD0 PRELIMINARY; PRT; 239 AA.
 AC Q8TCD0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH2362.1; -.
 DR PIR; S22658; S22658.
 DR PIR; S34095; S34095.
 DR PIR; S40324; S40324.
 DR PIR; S40374; S40374.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR HSP; P01834; 1172.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;
 Query Match 75.6%; Score 518.5; DB 2; Length 239;
 Best Local Similarity 73.7%; Pred. No. 8.6e-45;
 Matches 98; Conservative 19; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MKLPVRLLL-VLMFWIPASNSDVLMTQSPSLPSVSLGDSQASISCRSSQSIIVHNGDTYLEW 59
 DB 1 MKLPVRLLL-VLMFWIPASNSDVLMTQSPSLPSVSLGDSQASISCRSSQSIIVHNGDTYLEW 60
 QY 60 YLQKPGQSPKLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVYP 119
 DB 61 FQQRPGQSPRLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCMQGTHWP 120
 QY 120 YAFGGGTGLEIKR 132
 DB 121 STFGQGTGLEIKR 133
 RESULT 4
 KV2P_HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86041852; PubMed=2997711;
 RX Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 III";
 RL Nucleic Acids Res. 13:6499-6513(1985).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; Z00020;	CAA77315.1; -
DR	
PTIR; A01890;	K2HURP.
DR	
HSSP; Q9NM37;	I191.
DR	
GO; GO:0005763;	C:extracellular; NAS.
DR	
GO; GO:0003823;	F:antigen binding; NAS.
DR	
GO; GO:0006955;	P:immune response; NAS.
DR	
InterPro; IPR007110;	IG-like.
DR	
InterPro; IPR003596;	IG_v.
DR	
Pfam; PF000047;	ig; 1.
DR	
SMART; SMO0406;	IGv; 1.
DR	
PROSITE; PS00835;	IG_LIKE; 1.
DR	
KW	Immunoglobulin V region; Signal.
SIGNAL	1 20
FT CHAIN	21 133
FT DOMAIN	21 43
FT DOMAIN	44 59
FT DOMAIN	60 74
FT DOMAIN	75 81
FT DOMAIN	82 113
FT DOMAIN	114 122
FT DOMAIN	123 132
FT DISULFID	43 113
FT NON TER	133 133
SQ SEQUENCE	133 AA; 14707 MW; 513CCAF3673009BE CRC64;

Query Match	75.0%;	Score 514.5;	DB 1;	Length 133;
Best Local Similarity	72.9%;	Pred. No. 1.le-44;		
Matches 97;	Conservative 20;	Mismatches 15;	Indels 1;	Gaps 1;
Qy	1	MKLPVRL--VLMEFI PASNSDVLMTQPSLIPVSLGDOASICRSCSSOSIVHSNGDVTLEW	59	
Db	1	MRUPAQGLGLMLVPGSSGVVMTQPSLVPVLGQPASICRSCSSOSLVSGNTYLNW	60	
Qy	60	YLQKPGQSKLLIYKVSDRPSGVPDRFSGSGSGTDFTLKISRVEAEDLGVVFCQGSHP	119	
Db	61	FQRPQGSPPRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDGVVYCMQGTWS	120	
Qy	120	YAFGGGTYKLEIKR	132	
Db	121	WTFQGTQVEIKR	133	

```

RESULT 5
Q65ZCO
ID Q65ZCO PRELIMINARY; PRT; 219 AA.
AC Q65ZCO;
DT 25-OCT-2004 (TREMBlurel. 28, Created)
DT 25-OCT-2004 (TREMBlurel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlurel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP RC STRAIN=Balb/c; TISSUE=Spleen;
RA MEDLINE=96319505; PubMed=8768802;
RX Kipp B., Schlaak M., Becker W.M.;
RT "cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t.1";
RL Int. Arch. Allergy Immunol. 110:348-353(1996) .
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig CI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig V.

```

DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00635; IG-LIKE; 2.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 73.6%; Score 505; DB 2; Length 219;
Best Local Similarity 85.8%; Pred. No. 1.9e-43;
Matches 97; Conservative 8; Mismatches 8; Indels 0; Gaps

QY 20 DVLMTQSPLSLVSIGDQASISCRSSQSIHVSNGDTYLEWYLOKPGSPKLLIYKYSDRF
DB 1 ELVMTQSPLSLVSIGDQASISCRSSQSLVHNGNTYHLWYLOKPGSPKLLIYVNSRF
QY 80 SGVPRDFSGSGSGTDTFLKISRVEAEDLGVYFCFGSGHVPYAFGGGTKLEIKR 132
DB 61 SGVPRDFSGSGSGTDTFLKISRVEAEDLGVYFCFSQSTHVPGTFCGGTKEIKR 113

RESULT 6

ID Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
PC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Shen M.C., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
PC SEQUENCE FROM N.A.
PC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR

```

DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 72.5%; Score 497.5; DB 2; Length 239;
Best Local Similarity 69.2%; Pred. No. 1.2e-42;
Matches 92; Conservative 22; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRL-LVLMFWIPASNSDVLMTQSPLSPLVSLGDAQISICRSQSIVHNGDTYLEW 59
Db 1 MRLLAQLGLLMLWVPGSGDIVMTQTPLSSPTVLGQPASISCRSSSELHNGNTYLSW 60
QY 60 YLQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVP 119
Db 61 LHQRPGQPPRLIYKISNRFSGVDPDRFSGSGAGTFTLKISRVEAEDVGVYTCMQVSHFP 120
QY 120 YAFGGGTGLEIKR 132
Db 121 RTFGQGTVEIKR 133

RESULT 7
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; Ig-like.

```

```

DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 72.1%; Score 494.5; DB 2; Length 239;
Best Local Similarity 69.9%; Pred. No. 2.5e-42;
Matches 93; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

QY 1 MKLPVRL-LVLMFWIPASNSDVLMTQSPLSPLVSLGDAQISICRSQSIVHNGDTYLEW 59
Db 1 MRLPAQLGLLMLWVPGSGDIVMTQSPLSPLVFTGEPASISCRSSQSLHSDGNYLDM 60
QY 60 YLQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVP 119
Db 61 YLQKPGQSPQLLIYLGNSRAGVDPDRFSGSGGTFTLKISRVEAEDVGIYTCMQGLQTP 120
QY 120 YAFGGGTGLEIKR 132
Db 121 QTFGQGTVEIKR 133

RESULT 8
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KBS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

```

```

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 70.0%; Score 480; DB 2; Length 240;
Best Local Similarity 70.1%; Pred. No. 7.6e-41;
Matches 94; Conservative 16; Mismatches 22; Indels 2; Gaps 2;

Oy 1 MKLPVRLIL-VLMFWIPASNSDLVMTQSPSLSPVSLGDAQSISCRSSOSIVHSNGDTYLEW 59
Db 1 MRLPAQLGLMLVSGSGDIVMAQSPSLSPVTPGEPASISCRSSQSLLSHNGVYFDW 60

Oy 60 YLQKPGQSPKLLIYKVDVRFSGVDRFSGSGGTDFTLKISRVAEDLGVYFCFGSHV- 118
Db 61 YLQKPGQSPQLLIYGNRSGVDRFSGSGGTDFTLKISRVAEDLGVYFCFGSHV- 120

Oy 119 PYAFGGTKLEIKR 132
Db 121 PYTFGGTKLEIKR 134

RESULT 9
KV2E_HUMAN
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76 (1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.

FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 66.5%; Score 456; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 9.2e-39;
Matches 87; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Oy 17 SNSDLMTQSPSLSPVSLGDAQSISCRSSOSIVHSNGDTYLEWYLOKPGQSPKLLIYKVS 76
Db 2 SSGDIVMTQSPSLSPVTPGEPASISCRSSQSLLSHNGVYLDWYLOKPGQSPQLLIYLG 61

Oy 77 DRFSGVDRFSGSGGTDFTLKISRVAEDLGVYFCFGSHVPAFAGGTTKLEIKR 132
Db 62 NRASGVDRFSGSGGTDFTLKISRVAEDLGVYFCFGSHVPAFAGGTTKLEIKR 117

RESULT 10
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
Primary amyloidosis.";
RL Biochemistry 12:3763-3780 (1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Oserman E.F.;
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281 (1973).
CC -1- MISCELLANEOUS: The major amyloid protein appears to be identical
CC with the Bence Jones protein isolated from the same patient.
CC -1- MISCELLANEOUS: This protein was isolated from the urine of a
CC patient with plasma cell dyscrasia and amyloidosis.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
DR PIR; A90370; K2HUTW.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.

```



```
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12330 MW; 4E93797046F8DB33 CRC64;

Query Match 63.3%; Score 434; DB 1; Length 113;
Best Local Similarity 71.7%; Pred. No. 1.6e-36;
Matches 81; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 20 DVLMTQSPSLSPVSLGDOASISCRSSQSIHVSNGDTYLEWYLPKPGQSPKLLIYKVSDFR 79
Db 1 DIVMTQAVFSPNVTIGTSASISCRSKSLHNSGITYLYWYLPKPGQSPQLLYQMSNLA 60

QY 80 SGVPRDFSGSGSGTDFTLKISRVEAEDLGVPFCFGSHVPYAFGGTKLEIKR 132
Db 61 SGVPRDFSSSGSGTDFTLISRVEAEDVGVIYCAHNLPLVTFGGTKLEIKR 113

RESULT 14
KV2A HUMAN
ID KV2A HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 119I.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 61.3%; Score 420.5; DB 1; Length 112;
Best Local Similarity 66.4%; Pred. No. 3.8e-35;
Matches 75; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

QY 20 DVLMTQSPSLSPVSLGDOASISCRSSQSIHVSNGDTYLEWYLPKPGQSPKLLIYKVSDFR 79
Db 1 DIVLTQSPSLSPVTPGEPASISCRSSQNLZSBGB-YLDWYLZKPGZSPZLLIYGSNRA 59

QY 80 SGVPRDFSGSGSGTDFTLKISRVEAEDLGVPFCFGSHVPYAFGGTKLEIKR 132
Db 60 SGVPRDFSGSGSGTDFTLKISRVAZBVGVIYCAHNLPLVTFGGTKLEIKR 112

Search completed: May 25, 2005, 15:56:06
Job time : 64.3423 secs
```

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 65.427 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773A-17
Perfect score: 726
Sequence: 1 MNFGLSLFLVLKVGQCE.....HSVGCWFATWGGTLVTVSA 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	726	100.0	139	6	ABG74247
2	590	81.3	133	6	ABG74243
3	581	80.0	137	2	AAW57592
4	581	80.0	137	2	AAW89625
5	581	80.0	137	3	AAW77513
6	581	80.0	137	4	AAW67102
7	581	80.0	137	4	AAW64775
8	581	80.0	137	4	AAW63393
9	581	80.0	137	5	ABW95208
10	581	80.0	137	5	ABJ36667
11	581	80.0	137	8	ADO33883
12	578.5	79.7	138	2	AAW20064
13	578.5	79.7	138	8	ADR88408
14	577.5	79.5	138	5	ABG76924
15	562.5	77.5	144	5	ABW79730
16	555	76.4	141	8	ADO43551
17	554	76.3	139	2	AAW52773
18	554	76.3	139	2	AAW52791
19	553.5	76.2	140	6	ABG74241
20	553.5	76.2	142	2	AAW30982
21	552	76.0	141	8	ADO43555
22	550.5	75.8	136	2	AAW06251
23	546	75.2	139	2	AAW21656
24	543	74.8	140	2	AAW21654
25	542.5	74.7	138	2	AAW32246

26	542.5	74.7	138	2	AAW32242
27	542.5	74.7	139	2	AAW31588
28	542.5	74.7	462	6	AAO29869
29	542.5	74.7	462	7	ADJ79787
30	542.5	74.7	464	5	AAU72801
31	541.5	74.6	138	8	ADR47397
32	541	74.5	471	8	ADM72029
33	538.5	74.2	144	8	ADR47417
34	534.5	73.6	138	5	ABG76928
35	534.5	73.6	138	8	ADR88412
36	534.5	73.6	477	2	AAW47450
37	534.5	73.6	477	2	AAW47453
38	534	73.6	139	2	AAW52823
39	534	73.6	139	2	AAW70471
40	533.5	73.5	138	4	AAW67665
41	533.5	73.5	138	6	ABR40284
42	533.5	73.5	468	6	ABP58275
43	532.5	73.3	138	5	ABG76932
44	532.5	73.3	138	8	ADR88416
45	531.5	73.2	136	2	AAW56962

ALIGNMENTS

RESULT 1
ABG74247

ID ABG74247 standard; protein; 139 AA.

AC ABG74247;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3E11 heavy chain variable region.

XX

T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CDalpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

PN US2002132983-A1.

XX 19-SEP-2002.

PD 10-DEC-2001; 2001US-00006773.

PF 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

PI Junghans RP;

XX WPI; 2003-208946/20.

DR N-PSDB; ABX16573.

XX New chimera molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.

PS Disclosure; Page 17; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GD3 (ganglioside antigen) binding domain of antibody MB3.6, with any of 3 variable gene sequences, or the PSMA (prostate-specific membrane antigen) binding domain of antibody 3D8, 4D4 and 3E11, with variable gene sequences, the zeta signalling chain of the T cell receptor and an intervening CD8alpha hinge in which cysteine residues have been mutated. The chimaeric molecules expressed in T cells or NK cells or other effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3E11 heavy chain variable region
 XX
 SQ Sequence 139 AA;

Query Match 100.0%; Score 726; DB 6; Length 139;
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60
 DB 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60
 QY 61 DKRLWVASISTGGANTFYPDNVKGRTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
 DB 61 DKRLWVASISTGGANTFYPDNVKGRTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
 QY 121 SVGCWFATWGQGLTVTVSA 139
 DB 121 SVGCWFATWGQGLTVTVSA 139

RESULT 2
 ABG74243
 ID ABG74243 standard; protein; 133 AA.
 AC ABG74243;

22-APR-2003 (first entry)

Mouse antibody 3D8 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;
 KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
 KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
 KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
 KW small cell lung cancer; heavy chain variable region; mouse.

XX Mus sp.

XX US2002132983-A1.

XX 19-SEP-2002.

XX 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Junghans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16569.

XX New chimeric molecule useful in treating patients with disorders, such as
 PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
 PT comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 12; 35pp; English.

XX The invention relates to a chimeric molecule comprising the GD3
 CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
 CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
 CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
 CC sequences, the zeta signalling chain of the T cell receptor and an
 CC intervening CD8alpha hinge in which cysteine residues have been mutated.

CC The chimaeric molecules expressed in T cells or NK cells or other
 CC effector cells are useful in treating patients with cancers expressing
 CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3D8 heavy chain variable region
 XX
 SQ Sequence 133 AA;

Query Match 81.3%; Score 590; DB 6; Length 133;
 Best Local Similarity 83.5%; Pred. No. 6.6e-47;
 Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;
 QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60
 DB 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFTFSNYGMSWVRQTS 60
 QY 61 DKRLWVASISTGGANTFYPDNVKGRTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
 DB 61 DKRLWVASISSGGSTFYADNVKGRFTISRANKNTLYLQMSLSKSEDTALYFCARDH- 119
 QY 121 SVGCWFATWGQGLTVTVSA 139
 DB 120 ----LFWNGQGLTVTVSS 133

RESULT 3
 AAW57592
 ID AAW57592 standard; protein; 137 AA.
 AC AAW57592;

03-SEP-1998 (first entry)

Chimeric antibody against hPTRP H chain V region SEQ ID NO:57.

XX Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphataemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised.

XX Synthetic.

XX Mus sp.

XX Homo sapiens.

XX Chimeric.

XX WO9813388-A1.

XX 02-APR-1998.

XX 24-SEP-1997; 97WO-JP003382.

XX 26-SEP-1996; 96JP-00255196.

XX 24-JUL-1997; 97JP-00214168.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Sato K, Wakahara Y, Yabuta N;

XX WPI; 1998-230640/20.

XX N-PSDB; AAV24232.

XX New chimeric antibodies against human parathormone related peptide(s) -
 PT useful for, e.g. treatment of hypercalcaemia and other disorders caused
 PT by malignant neoplasm(s).

XX Claim 52; Page 120-121; 182pp; Japanese.

XX New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric L

CC and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They may
 CC also be used for treatment of hypophosphataemia such as that due to
 CC pathogens or to vitamin D resistance

XX Sequence 137 AA;

Query Match 80.0%; Score 581; DB 2; Length 137;
 Best Local Similarity 79.1%; Pred. No. 4.7e-46;
 Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;
 Qy 1 MNFGLSLIFLVLKGVQCEVKLVESGDLNMPGASLKLSCAAGFSFSNYGMSWVROTS 60
 Db 1 MNFGLSLIFLALILKGVQCEVQLVSGDLVKGPGSLKLSCAAGFTFSSYGMWIRQTP 60
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
 Db 61 DKRLWVASISTGGSYTYPPDSVKGRTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120
 Qy 121 SVGCWFATWGQGLTVTVSA 139
 Db 121 MT--YFAYWGQGLTVTVSA 137

RESULT 4

AAW89625
 ID AAW89625 standard; protein; 137 AA.

AC AAW89625;

DT 14-APR-1999 (first entry)

XX Mouse humanised antibody #23-57-137-1 heavy chain protein.

DE Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW inhibitor; humanised.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide

FT 1..19 /label= signal

FT Protein

XX 20..137

XX WO9851329-A1.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-JP002116.

XX PR 15-MAY-1997; 97JP-00125505.

XX PR 18-JUL-1997; 97JP-00194445.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Tunenari T, Ishii K;

XX DR WPI; 1999-070101/06.

XX DR N-ESDB; AAX00092.

XX Inhibitors of binding of parathyroid hormone related peptide to its
 PT receptor - useful for, e.g. treatment of cachexia arising from cancer or
 PT other diseases.

XX Example 2; Page 82; 125pp; Japanese.

XX

CC The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an active
 CC component. This substance may be an antagonist to the receptor, or an
 CC antibody (preferably monoclonal) or antibody fragment, recognising PTHrP.
 CC The antibody is preferably humanised or chimeric. The present invention
 CC also describes a humanised antibody prepared by hybridoma 23-57-137-1
 CC (FERM BP-5631). The composition is used for the treatment of cachexia
 CC arising in connection with diseases such as cancer, thereby improving the
 CC quality of life of the patient. The present sequence represents mouse
 CC humanised antibody heavy chain from #23-57-137-1 from the present
 CC invention

XX Sequence 137 AA;

Query Match 80.0%; Score 581; DB 2; Length 137;
 Best Local Similarity 79.1%; Pred. No. 4.7e-46;
 Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;
 Qy 1 MNFGLSLIFLVLKGVQCEVKLVESGDLNMPGASLKLSCAAGFSFSNYGMSWVROTS 60
 Db 1 MNFGLSLIFLALILKGVQCEVQLVSGDLVKGPGSLKLSCAAGFTFSSYGMWIRQTP 60
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
 Db 61 DKRLWVASISTGGSYTYPPDSVKGRTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120
 Qy 121 SVGCWFATWGQGLTVTVSA 139
 Db 121 MT--YFAYWGQGLTVTVSA 137

RESULT 5

AAW77513

ID AAY77513 standard; protein; 137 AA.

AC AAY77513;

DT 26-APR-2000 (first entry)

XX Mouse antibody H chain V region.

DE Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

XX Mus musculus.

XX WO200000219-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-JP003433.

XX PR 26-JUN-1998; 98JP-00180143.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Tsunenari T;

XX DR WPI; 2000-117115/10.

XX DR N-ESDB; AAZ58913.

XX Treatment of hypercalcaemic crisis with a substance inhibiting binding of
 PT parathyroid hormone related peptide to its receptor.
 XX Example 2; Page 96-97; 120pp; Japanese.

XX The invention relates to a method of treatment of hypercalcaemic crisis. A

XX composition for the treatment of hypercalcaemic crisis contains as active
 CC component a substance which inhibits the binding of parathyroid hormone
 CC related peptide (PTHrP) to its receptor. The inhibitor is used for the
 CC treatment of hypercalcaemic crisis, such as that associated with a
 CC malignant tumour

XX

4

CC analgesic. The present sequence represents the heavy chain variable
CC region (VH) precursor of anti-human PTHrP murine monoclonal antibody 23-
CC 57-137-1
XX
SQ Sequence 137 AA;

Query Match 80.0%; Score 581; DB 4; Length 137;
Best Local Similarity 79.1%; Pred. No. 4.7e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
DB 61 DKRLWVASISTGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120
QY 121 SVGCWFATWGQGLTVTVSA 139
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 8
AAG63393
ID AAG63393 standard; protein; 137 AA.
AC AAG63393;
XX
DT 15-OCT-2001 (first entry)
XX
DE Amino acid sequence of a murine polypeptide.
XX
KW Parathyroid hormone-associated peptide; PTHrP; dental disease.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 20..137
FT /note= "mature protein"
XX
PN WO200154725-A1.
XX
PD 02-AUG-2001.
XX
PE 14-DEC-2000; 2000WO-JP008875.
XX
PR 25-JAN-2000; 2000JP-00083034.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Kato A, Suzuki M, Sugimoto T;
XX
DR WPI; 2001-465459/50.
XX
DR N-PSDB; AAH74284.
XX
PT Parathyroid hormone-associated peptide binding inhibitors useful for
PT treating dental disease.
XX
PS Disclosure; Page 111-112; 140pp; Japanese.
XX
CC The specification describes a treatment for dental diseases. The
CC treatment comprises a substance that inhibits binding between parathyroid
CC hormone-associated peptide and its receptor. The present sequence
CC represents a murine protein, which is used in the course of the invention
XX
SQ Sequence 137 AA;

Query Match 80.0%; Score 581; DB 4; Length 137;
Best Local Similarity 79.1%; Pred. No. 4.7e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
DB 61 DKRLWVASISTGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120
QY 121 SVGCWFATWGQGLTVTVSA 139
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 9
ABB95208
ID ABB95208 standard; protein; 137 AA.
AC ABB95208;
XX
DT 17-JUN-2002 (first entry)
XX
DE Mouse joint disease realted protein SEQ ID NO 57.
XX
KW Joint disease; PTH; PTHrP; parathyroid hormone-related peptide;
KW parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.
XX
OS Mus musculus.
XX
PN WO200213865-A1.
XX
PD 21-FEB-2002.
XX
PE 15-AUG-2001; 2001WO-JP007044.
XX
PR 16-AUG-2000; 2000JP-00247013.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Yoshikawa H;
XX
DR WPI; 2002-257551/30.
XX
DR N-PSDB; ABL94765.
XX
PT Agents for ameliorating symptoms caused by joint diseases relating to PTH
PT or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors on
PT receptor binding of parathyroid hormone-related peptide.
XX
PS Disclosure; Page 88-89; 112pp; Japanese.
XX
CC The invention relates to agents for ameliorating symptoms causing joint
CC diseases, containing a substance inhibiting the binding of a parathyroid
CC hormone-related peptide to its receptor as active ingredient. The agents
CC have osteopathic activity are useful for ameliorating symptoms caused by
CC joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis
CC and arthritis deformans. The agents particularly improve the lowering of
CC bone amount or suppression of bone reduction. The present sequence is
CC that of a joint disease related protein, useful to the invention
XX
SQ Sequence 137 AA;

Query Match 80.0%; Score 581; DB 5; Length 137;
Best Local Similarity 79.1%; Pred. No. 4.7e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVROT 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
DB 61 DKRLWVASISTGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120
QY 121 SVGCWFATWGQGLTVTVSA 139
DB 121 MT--YFAYWGQGLTVTVSA 137

```

Db      121 MT--YFAYWGQGLTVTUSA 137

RESULT 10
ABJ36667
ID      ABJ36667 standard; protein; 137 AA.
XX      AC
XX      ABJ36667;
XX      OS
XX      24-APR-2003 (first entry)
XX      DE
XX      Angiogenesis inhibitor related mouse protein of SEQ ID No 57.
XX      DE
XX      Cytostatic; osteopathic; angiogenesis inhibitor; antitumour agent;
XX      KW      bone metastasis inhibitor; parathyroid hormone-associated peptide; PTHrP;
XX      KW      cancer; bone metastasis; mouse; murine.
XX      OS
XX      Mus musculus.
XX      PN
XX      WO200292133-A1.
XX      PD
XX      21-NOV-2002.
XX      PF
XX      10-MAY-2002; 2002WO-JP004586.
XX      PR
XX      10-MAY-2001; 2001JP-00140659.
XX      PA
XX      (CHUS ) CHUGAI SEIYAKU KK.
XX      PI
XX      Saito H, Tsunenari T, Onuma E, Kato A, Suzuki M;
XX      WPI: 2003-120614/11.
XX      DR
XX      N-PSDB; AB731673.
XX      PT
XX      Angiogenesis inhibitors being substances capable of inhibiting binding of
XX      PT      parathyroid hormone-associated peptide to its receptor, applicable in
XX      PT      antitumor agents and bone metastasis inhibitors for clinical use.
XX      PS
XX      Example 5; Page 88; 110pp; Japanese.
XX      CC
XX      The invention relates to novel angiogenesis inhibitors or antitumour
XX      CC      agents, or bone metastasis inhibitors, as active ingredient substances
XX      CC      which inhibit the binding of a parathyroid hormone-associated peptide
XX      CC      (PTHrP) to its receptor. The angiogenesis inhibitors are applicable in
XX      CC      antitumour agents and bone metastasis inhibitors for clinical treatment
XX      CC      of cancer and bone metastasis. This sequence represents a mouse protein
XX      CC      relating to the parathyroid hormone-associated peptide binding inhibitors
XX      CC      of the invention
XX      SQ
XX      Sequence 137 AA;

Query Match      80.0%; Score 581; DB 6; Length 137;
Best Local Similarity 79.1%; Pred. No. 4.7e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY      1 MNFGSLIFLVLKGVQCEVKLVESGDLMPGASLKLSCAASGFSFSGNYGMSWVROT 60
DB      1 MNFGSLIFLVLKGVQCEVKLVESGDLMPGASLKLSCAASGFSFSGNYGMSWVROT 60
QY      61 DKRLEWVASISTGGANTFYPDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
DB      61 DKRLEWVASISSGGSYTYPPDSVKGRFTISRANAKNTLYLQMSLSKSEDTAMFYCARQTT 120
QY      121 SVGCWFATWGQGLTVTUSA 139
DB      121 MT--YFAYWGQGLTVTUSA 137

RESULT 11
ADO33883
ID      ADO33883 standard; protein; 137 AA.
XX      AC
XX      ADO33883;
XX      AC

```

```

XX      26-AUG-2004 (first entry)
XX      DE
XX      Murine parathyroid hormone-related peptide-related precursor protein 1.
XX      KW      chondroma; chondrosarcoma; parathyroid hormone-related peptide; PTHrP;
XX      KW      cytostatic; apoptosis; house mouse; murine; precursor.
XX      OS
XX      Mus musculus.
XX      FH
XX      Key
XX      Peptide      1..19
XX      FT      /label= Signal_peptide
XX      FT      Protein      20..137
XX      FT      /note= "Murine parathyroid hormone-related peptide
XX      FT      (PTHrP)-related mature protein 1"
XX      PN
XX      WO2004045643-A1.
XX      PD
XX      03-JUN-2004.
XX      PF
XX      22-AUG-2003; 2003WO-JP010627.
XX      PR
XX      18-NOV-2002; 2002JP-00334081.
XX      PA
XX      (CHUS ) CHUGAI SEIYAKU KK.
XX      PI
XX      Yoshikawa H, Miyaji T;
XX      WPI: 2004-431847/40.
XX      DR
XX      N-PSDB; ADO33854.
XX      PT
XX      Novel therapeutic agent for chondroma and chondrosarcoma, having antibody
XX      PT      to parathyroid hormone related peptide (PTHrP) that inhibits binding of
XX      PT      PTHrP to its receptor, for inducing apoptosis in chondroma and
XX      PT      chondrosarcoma cell.
XX      PS
XX      Disclosure; Page 114; 143pp; Japanese.
XX      CC
XX      The invention relates to a novel therapeutic agent for chondroma and
XX      CC      chondrosarcoma comprising a substance that inhibits binding of
XX      CC      parathyroid hormone-related peptide (PTHrP) to its receptor. The agent of
XX      CC      the invention demonstrates cytostatic activity and may be useful for
XX      CC      inducing apoptosis in chondroma and chondrosarcoma cells, thus
XX      CC      effectively treating chondroma and chondrosarcoma. The agent is specific
XX      CC      to human PTHrP. The current sequence is that of a murine PTHrP-related
XX      CC      precursor protein which is shown in the sequence listing of the
XX      CC      invention.
XX      SQ
XX      Sequence 137 AA;

Query Match      80.0%; Score 581; DB 8; Length 137;
Best Local Similarity 79.1%; Pred. No. 4.7e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY      1 MNFGSLIFLVLKGVQCEVKLVESGDLMPGASLKLSCAASGFSFSGNYGMSWVROT 60
DB      1 MNFGSLIFLVLKGVQCEVKLVESGDLMPGASLKLSCAASGFSFSGNYGMSWVROT 60
QY      61 DKRLEWVASISTGGANTFYPDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
DB      61 DKRLEWVASISSGGSYTYPPDSVKGRFTISRANAKNTLYLQMSLSKSEDTAMFYCARQTT 120
QY      121 SVGCWFATWGQGLTVTUSA 139
DB      121 MT--YFAYWGQGLTVTUSA 137

RESULT 12
AAR20064
ID      AAR20064 standard; protein; 138 AA.
XX      AC
XX      AAR20064;
XX      AC

```

```

XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1992 (first entry)
XX MRK16-H chain.
XX Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX Homo; sapiens.
OS Mus musculus.
OS Chimeric.
XX JP03254691-A.
XX 13-NOV-1991.
XX 02-MAR-1990; 90JP-00051563.
XX 02-MAR-1990; 90JP-00051563.
XX (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX WPI; 1992-002461/01.
DR N-PSDB; AAQ20070.
XX Chimera antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX Disclosure; Fig 4; 20pp; Japanese.
XX A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX Sequence 138 AA;
Query Match 79.7%; Score 578.5; DB 2; Length 138;
Best Local Similarity 79.9%; Pred. No. 8e-46;
Matches 111; Conservative 14; Mismatches 13; Indels 1; Gaps 1;
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVROTP 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 EKRLWVATISSGGNTYPPSVKGRFTISRDNAKNNLYLQMSLSRSDTALYFCAR-YY 119
Qy 121 SVGCWFATWGQGLTVTUSA 139
Db 120 RYEAWFASWGQGLTVTUSA 138
RESULT 13
ADR88408
ID ADR88408 standard; protein; 138 AA.
XX AC ADR88408;
XX 16-DEC-2004 (first entry)
DT Murine 3D6 immunoglobulin heavy chain variable region SEQ ID NO:4.
DE

```

```

XX 3D6; heavy chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; neurotropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX Mus musculus.
XX Key Location/Qualifiers
FH 1.19
FT /label= signal peptide
FT Protein 20..138
FT /label= mature protein
XX WO2004080419-A2.
XX 23-SEP-2004.
XX 12-MAR-2004; 2004WO-US007503.
XX 12-MAR-2003; 2003US-00388389.
XX (NEUR-) NEURALAB LTD.
PA (AMHP ) WYETH.
XX Basi G, Saldanha JW, Yednock T;
XX WPI; 2004-668880/65.
DR N-PSDB; ADR88407.
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX Claim 2; SEQ ID NO 4; 176pp; English.
XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 3D6
CC immunoglobulin heavy chain variable region.
XX Sequence 138 AA;
Query Match 79.7%; Score 578.5; DB 8; Length 138;
Best Local Similarity 82.7%; Pred. No. 8e-46;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVROTS 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 DKRLWVASIRSGGRTYSDNVKGRFTISRENKNTLYLQMSLSKSDTALYFCARDYDH 120

```


Qy 121 SVGWFAT--WGQGLVTUSA 139
Db 121 SYGSIYYAMDYWGQGLVTSS 142

Search completed: May 25, 2005, 15:47:22
Job time : 66.427 secs

BEST AVAILABLE COPY

RESULT 3
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew

RESULT 4
US-08-376-183A-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A333
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 925853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-31

Query Match 74.4%; Score 540.5; DB 3; Length 136;
Best Local Similarity 76.3%; Pred. No. 7.5e-51;
Matches 106; Conservative 16; Mismatches 14; Indels 3; Gaps 1

QY 1 MNFGLSLFLVLVLKGVQCEVKLVESGGDLMNPGASLKLSCAAGGFSPNYGMSWVROTS 60
Db 1 MNFGLSLFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAAGGFAPSTYDMSWVROTP 60
QY 61 DKLEWVASISTGCATFYPDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 EKLEWVATISSGGSYYTLLDSVKGRFTISRSARNTLYLQMSLSRSEDTALYYCA---P 117
QY 121 SVGCWFATWGQGLTVTVSA 139
Db 118 TTVVPEAYWGQGLTVTVSA 136

```

```

Sequence 34, Application US/089/6183A
Patent No. 6307026
GENERAL INFORMATION:
APPLICANT: King, David J.
APPLICANT: Adair, John R.
APPLICANT: Owens, Raymond J.
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,183A

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/595,848

FILING DATE: 02-FEB-1996

APPLICATION NUMBER: PCT/GB93/02529

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: GB 9225853.2

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9315249.4

FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bernhard D. Saxe

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 40283/151/CARA

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-976-183A-32

Query Match 74.0%; Score 537.5; DB 3; Length 136;
Best Local Similarity 76.3%; Pred. No. 1.6e-50;
Matches 106; Conservative 15; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTS 60

Db 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120

Db 61 EKRLWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSLSRSEDALYYCA---P 117

QY 121 SVGCWFPATWGQGLTVTUSA 139

Db 118 TTVPFAYWGQGLTVTUSA 136

RESULT 7

US-08-976-183A-34

Sequence 34, Application US/08976183A

Patent No. 6307026

GENERAL INFORMATION:

APPLICANT: King, David J.

APPLICANT: Agair, John R.

APPLICANT: Owens, Raymond J.

TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K. Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,183A

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595,848
FILING DATE: 02-FEB-1996
APPLICATION NUMBER: PCT/GB93/02529
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-183A-34

Query Match 73.9%; Score 536.5; DB 3; Length 136;
Best Local Similarity 75.5%; Pred. No. 2e-50;
Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTS 60

Db 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120

Db 61 EKRLWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSLSRSEDALYYCA---P 117

QY 121 SVGCWFPATWGQGLTVTUSA 139

Db 118 TTVPFAYWGQGLTVTUSA 136

RESULT 8

US-08-253-877C-57

Sequence 57, Application US/08253877C

Patent No. 5773001

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.

APPLICANT: Hinman, Lois

APPLICANT: Hollander, Irwin

APPLICANT: Holcomb, Ryan

APPLICANT: Hallett, William

APPLICANT: Tsou, Hwei-Ru

APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza

CITY: Wayne

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 73.8%; Score 535.5; DB 1; Length 136;
Best Local Similarity 75.5%; Pred. No. 2.6e-50;
Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGSLKLSCAASGFSPSNYGMWVRQTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGLVPGGSLKLSCAASGFAPFTYDMSWVRQTP 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 EKRLWVATISSGGSYTYLLDSVKGRFTISRNTLYLQMSLSRSEDTALYYCA---P 117
Qy 121 SVGCWFATWGGTTLVTUSA 139
Db 118 TTVVPFAYWGGTTLVTUSA 136

RESULT 9
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 73.8%; Score 535.5; DB 1; Length 136;
Best Local Similarity 75.5%; Pred. No. 2.6e-50;
Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGSLKLSCAASGFSPSNYGMWVRQTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGLVPGGSLKLSCAASGFAPFTYDMSWVRQTP 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 EKRLWVATISSGGSYTYLLDSVKGRFTISRNTLYLQMSLSRSEDTALYYCA---P 117
Qy 121 SVGCWFATWGGTTLVTUSA 139
Db 118 TTVVPFAYWGGTTLVTUSA 136

RESULT 10
US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-129-930B-96

Query Match 73.6%; Score 534; DB 1; Length 139;
```

```

Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGGANTFYDPNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNVAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSSA 139
Db 121 GIPANFAYWGQGLTVTVSS 139

RESULT 11
US-08-134-346A-51
; Sequence 51, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Data L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-346A-51

Query Match 73.6%; Score 534; DB 3; Length 139;
Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGGANTFYDPNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNVAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSSA 139
Db 121 GIPANFAYWGQGLTVTVSS 139

```

```

Db 121 GIPANFAYWGQGLTVTVSS 139

RESULT 12
US-08-976-288A-96
; Sequence 96, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976-288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-976-288A-96

Query Match 73.6%; Score 534; DB 3; Length 139;
Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGGANTFYDPNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNVAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSSA 139
Db 121 GIPANFAYWGQGLTVTVSS 139

```



```
RESULT 13
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

Query Match 73.4%; Score 533; DB 3; Length 135;
Best Local Similarity 75.5%; Pred. No. 4.8e-50;
Matches 105; Conservative 15; Mismatches 15; Indels 4; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSNMGMSVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSNMGMSVROTS 60
Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 DKRLWVASISTGG-STYYPDSVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
Qy 121 SVGCWFATWGGTLTVTSSA 139
Db 121 G---YFDWVGQGTTLTVTSS 135

RESULT 14
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 73.1%; Score 530.5; DB 5; Length 247;
Best Local Similarity 74.8%; Pred. No. 1.9e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSNMGMSVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSNMGMSVROTS 60
Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 DKRLWVASISTGGGTYYPDNTVKGRFTISRDNKNTLYLQMSLSKSDTAMVHCARGGV 120
Qy 121 SVGCWFATWGGTLTVTSSA 139
Db 121 RRG-YFDWVGAGTTVTSS 138

RESULT 15
US-08-836-561-23
; Sequence 23, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
```

APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-836-561-23

Query Match 72.0%; Score 522.5; DB 3; Length 140;
Best Local Similarity 71.6%; Pred. No. 6.9e-49;
Matches 101; Conservative 20; Mismatches 17; Indels 3; Gaps 2;
QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVROTS 60
DB 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVROTS 60
QY 61 DKRLWVASITGGANTFYDPNVKGRFTISRENKNTLYLOMSSLKSEDTALVFCAQDSH 120
DB 61 DKRLWVASITGGANTFYDPNVKGRFTISRENKNTLYLOMSSLKSEDTALVFCAQDSH 120
QY 121 SVGCWFAT--WGQGLTVTVSA 139
DB 121 -YGNRYAMDYWGQGLTVTVSS 140

Search completed: May 25, 2005, 15:56:27
Job time : 18.3265 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 64.134 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773A-17
Perfect score: 726
Sequence: 1 MNFGLSLIFLVVLKGVQCE.....HSVGCWFWATWGQGLTVTUSA 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726	100.0	139	13	US-10-006-773-17
2	590	81.3	133	13	US-10-006-773-9
3	581	80.0	137	9	US-09-423-800-76
4	581	80.0	137	14	US-10-337-981-76
5	578.5	79.7	138	14	US-10-010-942B-4
6	578.5	79.7	138	15	US-10-388-389-4
7	578.5	79.7	138	16	US-10-703-713-4
8	578.5	79.7	138	16	US-10-704-070-4
9	578.5	79.7	138	17	US-10-232-030-4
10	562.5	77.5	144	9	US-09-881-823-12
11	553.5	76.2	140	13	US-10-006-773-4
12	542.5	74.7	462	14	US-10-281-479A-23
13	542.5	74.7	462	14	US-10-286-132A-23

14	542.5	74.7	464	14	US-10-275-180A-23	Sequence 23, Appl
15	534.5	73.6	138	14	US-10-010-942B-8	Sequence 8, Appl
16	534.5	73.6	138	15	US-10-388-389-8	Sequence 8, Appl
17	534.5	73.6	138	16	US-10-703-713-8	Sequence 8, Appl
18	534.5	73.6	138	16	US-10-704-070-8	Sequence 8, Appl
19	534.5	73.6	138	17	US-10-232-030-8	Sequence 8, Appl
20	534	73.6	139	10	US-09-947-839-96	Sequence 96, Appl
21	533.5	73.5	138	9	US-09-796-744-15	Sequence 15, Appl
22	533.5	73.5	138	14	US-10-231-452-62	Sequence 62, Appl
23	533.5	73.5	468	17	US-10-476-265-20	Sequence 20, Appl
24	532.5	73.3	138	14	US-10-010-942B-12	Sequence 12, Appl
25	532.5	73.3	138	15	US-10-388-389-12	Sequence 12, Appl
26	532.5	73.3	138	16	US-10-703-713-12	Sequence 12, Appl
27	532.5	73.3	138	16	US-10-704-070-12	Sequence 12, Appl
28	532.5	73.3	138	17	US-10-232-030-12	Sequence 12, Appl
29	525.5	72.4	140	9	US-09-286-240-4	Sequence 4, Appl
30	522.5	72.0	140	14	US-10-283-349-23	Sequence 23, Appl
31	515	70.9	137	9	US-09-423-800-77	Sequence 77, Appl
32	515	70.9	137	14	US-10-337-981-77	Sequence 77, Appl
33	512.5	70.6	158	15	US-10-226-795-32	Sequence 32, Appl
34	509.5	70.2	143	15	US-10-469-304-17	Sequence 17, Appl
35	501	69.0	467	15	US-10-180-648-2	Sequence 2, Appl
36	499	68.7	143	10	US-09-791-551-117	Sequence 117, App
37	497	68.5	177	16	US-10-693-629-64	Sequence 64, App
38	495.5	68.3	313	15	US-10-291-265-427	Sequence 427, App
39	493.5	68.0	159	15	US-10-291-265-333	Sequence 333, App
40	493	67.9	124	10	US-09-518-737-2	Sequence 2, Appl
41	493	67.9	124	17	US-10-723-748-2	Sequence 2, Appl
42	493	67.9	477	15	US-10-291-265-395	Sequence 395, App
43	492	67.8	118	9	US-09-423-800-46	Sequence 46, Appl
44	492	67.8	118	14	US-10-182-018-46	Sequence 46, Appl
45	492	67.8	118	14	US-10-169-003-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-10-006-773-17
; Sequence 17, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Jughans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-17

Query Match	100.0%;	Score 726;	DB 13;	Length 139;
Best Local Similarity	100.0%;	Pred. No. 2.2e-59;		
Matches 139;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MNFGLSLIFLVVLKGVQCEVKLVESGGDLNPGASLKLSCAASGFSPSYNGMSWVROTS	60	
Db	1	MNFGLSLIFLVVLKGVQCEVKLVESGGDLNPGASLKLSCAASGFSPSYNGMSWVROTS	60	
Qy	61	DKRLWVASISTGGANTFYPDNVKGRFTISRENAKNTLYQMSSLSKSEDTALYFCARDSH	120	
Db	61	DKRLWVASISTGGANTFYPDNVKGRFTISRENAKNTLYQMSSLSKSEDTALYFCARDSH	120	
Qy	121	SVGCWFWATWGQGLTVTUSA	139	
Db	121	SVGCWFWATWGQGLTVTUSA	139	

```

RESULT 2
US-10-006-773-9
; Sequence 9, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-9

Query Match      81.3%; Score 590; DB 13; Length 133;
Best Local Similarity 83.5%; Pred. No. 7.8e-47;
Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGLSLFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSSNYGMSWVRQTS 60
DB 1 MNFGLSLFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSSNYGMSWVRQTS 60

QY 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120
DB 61 DKRLEWVASISSGGDSTFFADNVKGRFTISRDNKNTLYLQMSLSKSEDTALFYCARDH- 119

QY 121 SVGCWFPATWGQGLTVTVSA 139
DB 120 ----LFNMGQGLTVTVSS 133

RESULT 3
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-76

Query Match      80.0%; Score 581; DB 9; Length 137;
Best Local Similarity 79.1%; Pred. No. 5.4e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSSNYGMSWVRQTS 60
DB 1 MNFGLSLFLALILKGVQCEQLVPGGSLKLSCAASGFTFSSYGMWIRQTP 60

QY 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120
DB 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120

QY 121 SVGCWFPATWGQGLTVTVSA 139
DB 120 ----LFNMGQGLTVTVSS 133

RESULT 4
US-10-006-773-9
; Sequence 76, Application US/10337981
; Publication No. US20030138424A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/10/337,981
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-76

Query Match      80.0%; Score 581; DB 14; Length 137;
Best Local Similarity 79.1%; Pred. No. 5.4e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSSNYGMSWVRQTS 60
DB 1 MNFGLSLFLALILKGVQCEQLVPGGSLKLSCAASGFTFSSYGMWIRQTP 60

QY 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120
DB 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120

QY 121 SVGCWFPATWGQGLTVTVSA 139
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 5
US-10-010-942B-4
; Sequence 4, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurij
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
```

```

Db 61 DKRLEWVASISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMFYCARQTT 120

QY 121 SVGCWFPATWGQGLTVTVSA 139
;
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 4
US-10-337-981-76
; Sequence 76, Application US/10337981
; Publication No. US20030138424A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/10/337,981
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-76

Query Match      80.0%; Score 581; DB 14; Length 137;
Best Local Similarity 79.1%; Pred. No. 5.4e-46;
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSSNYGMSWVRQTS 60
DB 1 MNFGLSLFLALILKGVQCEQLVPGGSLKLSCAASGFTFSSYGMWIRQTP 60

QY 61 DKRLEWVASISTGGANTFYPDNVKGRTTISRDNKNTLYLQMSLSKSEDTALFYCARDH 120
DB 61 DKRLEWVASISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMFYCARQTT 120

QY 121 SVGCWFPATWGQGLTVTVSA 139
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 5
US-10-010-942B-4
; Sequence 4, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurij
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
```

```

; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 14; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFSFNSYGMWSWRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFTFSNYGMWSWRQNS 60
Qy 61 DKLEWVASISTGCANTFYPDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWVASIRSGGRTYSDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCVRYDH 120
Qy 121 SVGCWPFATWGQGLTVTVSA 139
Db 121 YSGS-SDYWGQGTTVTVSS 138

RESULT 6
US-10-388-389-4
; Sequence 4, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 15; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFSFNSYGMWSWRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFTFSNYGMWSWRQNS 60
Qy 61 DKLEWVASISTGCANTFYPDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWVASIRSGGRTYSDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCVRYDH 120
Qy 121 SVGCWPFATWGQGLTVTVSA 139
Db 121 YSGS-SDYWGQGTTVTVSS 138

RESULT 7
US-10-703-713-4
; Sequence 4, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 16; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFSFNSYGMWSWRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFTFSNYGMWSWRQNS 60
Qy 61 DKLEWVASISTGCANTFYPDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWVASIRSGGRTYSDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCVRYDH 120
Qy 121 SVGCWPFATWGQGLTVTVSA 139
Db 121 YSGS-SDYWGQGTTVTVSS 138

RESULT 8
US-10-704-070-4
; Sequence 4, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-704-070-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 16; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFSFNSYGMWSWRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSAASGFTFSNYGMWSWRQNS 60
Qy 61 DKLEWVASISTGCANTFYPDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWVASIRSGGRTYSDNVKGRFTTISRENAKNTLYLQMSLSKSEDTALYFCVRYDH 120
Qy 121 SVGCWPFATWGQGLTVTVSA 139
Db 121 YSGS-SDYWGQGTTVTVSS 138

```

```

; EDUCATION NO: 0520004011613541
;
; GENERAL INFORMATION:
; APPLICANT: Bas1, Gur1q
; APPLICANT: Saldanha, Jose
;
; Query Match 79.7%; Score 578.5; DB 16; Length 138;
; Best Local Similarity 82.7%; Pred. No. 9.3e-46;
; Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1

```


Qy	121	SVGCWFAT--WGQGTFLVTVA	139
		: :	
Db	121	SM---ITTDYWGQGTTLTVSS	138

RESULT 15

US-10-010-942B-8

; Sequence 8, Application US/10010942B

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA AMYLOID PEPTIDE
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-8

Query Match 73.8%; Score 534.5; DB 14; Length 138;
Best Local Similarity 74.8%; Pred. No. 1.1e-41;
Matches 104; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFPSNYGMSWVROTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFPSNYGMSWVROTS 60
QY 61 DKLEWVASISTGGANTFYPDNVKGRFTISRENKNTLYLQMSLKSDEDTALYFCARDSH 120
Db 61 GKLEWVASIRSGGRTFYSDNVKGRFTISRDNAKNSLYLQMSLRAEDTALYVCVRYDH 120
QY 121 SVGCWFATWGQGTFLVTVA 139
Db 121 YSGS-SDYWGQGTFLVTSS 138

Search completed: May 25, 2005, 16:06:54
Job time : 65.259 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 19.654 Seconds
(without alignments)
680,480 Million cell updates/sec

Title: US-10-006-773A-17

Perfect score: 726

Sequence: 1 MNFGLSLIFLVVLKGVQCE.....HSVGCWFATWGQGLTVTUSA 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578.5	79.7	138	2 S09258	Ig heavy chain V r
2	547.5	75.4	142	2 C34903	Ig heavy chain pre
3	534.5	73.6	152	2 B26471	Ig heavy chain pre
4	528	72.7	139	2 S38808	Ig heavy chain - m
5	506	69.7	117	1 HVMS84	Ig heavy chain pre
6	503	69.3	117	1 HVMS34	Ig heavy chain pre
7	500	68.9	140	2 S70442	Ig heavy chain pre
8	495	68.2	117	1 HVMS39	Ig heavy chain pre
9	491	67.6	139	2 S31674	Ig heavy chain V r
10	491	67.6	254	2 B31790	Ig heavy chain V r
11	489.5	67.4	140	2 S31588	Ig heavy chain V r
12	488.5	67.3	138	2 S31666	Ig heavy chain V r
13	487	67.1	548	2 S38864	Ig epsilon chain C
14	481.5	66.3	140	2 A30532	Ig heavy chain pre
15	480.5	66.2	136	2 S31615	hypothetical prote
16	479.5	66.0	134	2 S31699	Ig heavy chain V r
17	479	66.0	117	1 HVMS57	Ig heavy chain pre
18	477.5	65.8	134	2 S31679	Ig heavy chain V r
19	477.5	65.8	140	2 S31686	Ig heavy chain V r
20	476	65.6	117	1 HVMSR	Ig heavy chain pre
21	475	65.4	137	2 S31701	Ig heavy chain V r
22	472	65.0	141	2 S31669	Ig heavy chain V r
23	471.5	64.9	140	2 S22657	Ig heavy chain V r
24	469.5	64.7	139	2 S27781	Ig heavy chain pre
25	469.5	64.7	160	2 S05271	Ig variable region
26	468	64.5	136	2 S31587	Ig heavy chain pre
27	467.5	64.4	130	2 PL0058	Ig heavy chain pre
28	467.5	64.4	135	2 S31598	Ig heavy chain V r
29	464.5	64.0	132	2 S31603	Ig heavy chain V r

30 463 63.8 135 2 I37778 Ig variable region
31 463 63.8 151 2 A60943 Ig heavy chain pre
32 462 63.6 121 2 D27888 Ig heavy chain V r
33 458.5 63.2 136 2 S60296 Ig heavy-chain var
34 458 63.1 147 2 I37780 Ig variable region
35 456 62.8 136 1 GIMS21 Ig heavy chain pre
36 453.5 62.5 136 2 S16847 Ig heavy chain V r
37 453.5 62.5 138 2 A30561 Ig heavy chain pre
38 453 62.4 137 2 S78054 Ig heavy chain pre
39 452 62.3 145 2 S11239 Ig heavy chain V r
40 451 62.1 119 2 D27889 Ig heavy chain V r
41 451 62.1 119 2 D27888 Ig heavy chain V r
42 451 62.1 128 2 PH0094 Ig heavy chain V r
43 450 62.0 119 2 PH1531 Ig H chain V regio
44 449.5 61.9 122 2 B27888 Ig heavy chain V r
45 448 61.7 118 2 PL0254 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C/Accession: S09258

R/Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A/Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK

A/Reference number: S09258; MUID:90245594; PMID:2110659

A/Accession: S09258

A/Molecule type: DNA

A/Residues: 1-138 <HAM>

A/Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

A/Genetics:

A/Introns: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 578.5; DB 2; Length 138;
Best Local Similarity 79.9%; Pred. No. 2.4e-45;
Matches 111; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVLSGSDLMNPGASLKLSCAASGFSFNYSVMSVWQTS 60

Db 1 MNFGLSLIFLVVLKGVQCEVLSGSDLMNPGASLKLSCAASGFTFSSYTMVSWVRQTP 60

Qy 61 DKRLWVASITGANTFFPDNVKGRFTISRENAKNTLYLQMSLSKSEDYALYFCARDSH 120

Db 61 EKRLWVATISSGGNTYYPDSVKGRFTISRDNAKNLYLQMSLSRSEDYALYFCAR-YY 119

Qy 121 SVGCWFATWGQGLTVTUSA 139

Db 120 RYFAWFASWGQGLTVTUSA 138

RESULT 2

C34903

Ig heavy chain precursor V region (5-27) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C/Accession: C34903

R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A/Title: Active site structure and antigen binding properties of idiotypically cross-re

A/Reference number: A34903; MUID:90094387; PMID:2104617

A/Accession: C34903

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-142 <BED>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 547.5; DB 2; Length 142;
Best Local Similarity 76.2%; Pred. No. 1.6e-42;
Matches 109; Conservative 12; Mismatches 17; Indels 5; Gaps 3;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60
DB 1 MNFGFSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLEWVASIS---TGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 117
DB 61 EKRLWVASFNGKPTCG-RTYYPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYCYCAR 119

QY 118 DSHSV-GCWFAWGGQTLTVSA 139
DB 120 GGYVGGYWFAYWGGQTLTVSA 142

RESULT 3
B26471
Ig heavy chain precursor V region (MAK33) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C;Accession: B26471; S70410
R;Buckel, P.; Hubner-Parajoz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A;Reference number: A91572; MUID:87248058; PMID:3110009
A;Accession: B26471
A;Molecule type: mRNA
A;Residues: 1-152 <BUC>
A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406
R;Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
A;Reference number: S70410; MUID:91079775; PMID:2258702
A;Accession: S70410
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <LEB>
A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476
C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;152/152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 534.5; DB 2; Length 152;
Best Local Similarity 74.6%; Pred. No. 2.6e-41;
Matches 106; Conservative 14; Mismatches 19; Indels 3; Gaps 1;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60
DB 1 MNFGFSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLEWVASIS---TGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 120
DB 61 EKRLWVATSDGSGTYTPYDPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYCARDKA 120

QY 121 SVGCW---FATWGGQTLTVSA 139
DB 121 YGNYGDAMDYWGQGTSTVTS 142

RESULT 4
S38808
Ig heavy chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S38808
R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.
Immunogenetics 36, 15-21, 1992
A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG
A;Reference number: S38807; MUID:92267566; PMID:1587549
A;Accession: S38808
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <SEQ>
A;Cross-references: EMBL:X53400
A;Note: the authors translated the codon GAG for residue 117 as Lys
A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 528; DB 2; Length 139;
Best Local Similarity 72.9%; Pred. No. 9.1e-41;
Matches 105; Conservative 14; Mismatches 13; Indels 12; Gaps 3;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60
DB 1 MNFGFSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLEWVASIS---TGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 120
DB 61 EKRLWVASISRGG-TTYYPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYCYCAR-- 117

QY 121 SVGCWFA-----TWGGQTLTV 137
DB 118 --GIYGYALYGMGYWGQGTSTV 139

RESULT 5
HWS84
Ig heavy chain precursor V region (5-84) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: J70505
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A;Reference number: J70501; MUID:89279149; PMID:2499654
A;Accession: J70505
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <LEV>
A;Cross-references: UNIPROT:P18525
A;Experimental source: strain BALB/cJ
A;Note: this sequence belongs to the VH7183 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 69.7%; Score 506; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 7.4e-39;
Matches 97; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60
DB 1 MNFGFSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLEWVASIS---TGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 117
DB 61 EKRLWVAYISNGGSGTYTPDVTKGRFTISRDNARNLYLQMSLSASEDTAMYCYCAR 117

RESULT 6
HWS34
Ig heavy chain precursor V region (345) - mouse
C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C;Accession: J70502

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A;Reference number: J70501; MUID:89279149; PMID:2499654

A;Accession: J70502

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Cross-references: UNIPROT:P18526

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;41-115/Disulfide bonds: #status predicted

Query Match 69.3%; Score 503; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 1.4e-38;
Matches 95; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60

Db 1 MNFGLRLFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAPSSYDMWVRQTP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCAR 117

Db 61 EKRLWVAYISSGGSTYPTPVTKGRFTISRDNKNTLYLQMSLSKSDTAMYYCAR 117

RESULT 7

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: S70442

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A;Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe

A;Reference number: S70442; MUID:93024508; PMID:1383695

A;Accession: S70442

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: UNIPROT:Q8WUK1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 500; DB 2; Length 140;
Best Local Similarity 68.6%; Pred. No. 3.1e-38;
Matches 96; Conservative 21; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60

Db 1 MEFGLSWFLVALLRGVQCQVQLVESGGVQVPGGSLRLSCAASGFTFSNGMHWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120

Db 61 GKLEWVAFIRYDGSNKYADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARD-H 119

Qy 121 SVGC-WFATWGGTTLVTUSA 139

Db 120 IVGATFYDYGQGTTLVTVSS 139

RESULT 8

HWS39

Ig heavy chain precursor V region (7-39) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

C;Accession: J70507

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A;Reference number: J70501; MUID:89279149; PMID:2499654

A;Accession: J70507

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Cross-references: UNIPROT:P18530

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (7-39) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;41-115/Disulfide bonds: #status predicted

Query Match 68.2%; Score 495; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 7.3e-38;
Matches 95; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60

Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGVKPGGSLKLSCEASGFTFSNYGMWVRQTP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCAR 117

Db 61 EKRLWVASISGGVSYTYYPDSVKGRFTISRDNKNTLYLQMSLSKSDTALYFCAR 117

RESULT 9

S31674

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31674

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31674

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <CUI>

A;Cross-references: EMBL:Z14204; NID:g30967; PIDN:CAA78573.1; PID:g30968

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 491; DB 2; Length 139;
Best Local Similarity 66.2%; Pred. No. 2e-37;
Matches 92; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60

Db 1 MEFGLSWFLVALLRGVQCQVQLVESGGVQVPGGSLRLSCAASGFTFSYGMHWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120

Db 61 CKGLEWVAVISYDGSNKYADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAKAGL 120

Qy 121 SVGCWFPATWGGTTLVTUSA 139

Db 121 GFFNWFDPWGGTTLVTVSS 139

RESULT 10

B31790

Ig heavy chain V region (17/9) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997

E;20-140/Product: Ig heavy chain V-III region 38 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 481.5; DB 2; Length 140;
Best Local Similarity 66.4%; Pred. No. 1.5e-36;
Matches 93; Conservative 21; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSNYGMGNVVRQTS 60
Db 1 MEFGLSLIFLVAILKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSNYGMGNVVRQAP 60

Qy 61 DKRLWVASISTGGANTYPDPNVKGRFTISRANAKNTLYLQWSSIKSDEDTALYFCARDSH 120
Db 61 KGLEWSSISGSGGTYTASVGRFTISRDNKNTLYLQWSSIKSDEDTALYFCARDNMG 120

Qy 121 SVGCW-FATWGQGLTVTVSA 139
Db 121 DIRLTPLAYWGQGLTVTVSS 140

RESULT 15
S31615
hypothetical protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31615
R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, April 1991
A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidiox
A;Reference number: S31615
A;Accession: S31615
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <REC>
A;Cross-references: EMBL:X58884; NID:G51824; PIDN:CAA41688.1; PID:G51825
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 480.5; DB 2; Length 136;
Best Local Similarity 66.2%; Pred. No. 1.8e-36;
Matches 94; Conservative 20; Mismatches 19; Indels 9; Gaps 3;

Qy 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSNYGMGNVVRQTS 60
Db 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSNYGMGNVVRQTP 60

Qy 61 DKRLWVASISTGGANTYPDPNVKGRFTISRANAKNTLYLQWSSIKSDEDTALYFCARDSH 120
Db 61 EKRLWVATITGGGTYTYPDSVGRFTISRDNARDTLNLHMTNLKSEDTAMYTC----- 115

Qy 121 SVGCW-FATWGQGLTVTVSA 139
Db 121 -LGYWYDGYWGQGLTVTVSA 136

Search completed: May 25, 2005, 16:48:41
Job time : 20.654 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 67.7544 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773A-17

Perfect score: 726

Sequence: 1 MNFGLSLIFLVVLKGVQCE.....HSVGCWFWTQGTGLVTUSA 139

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	75.6	487	Q99KA4	Q99ka4 mus musculus
2	528.5	72.8	486	Q91Z07	Q91z07 mus musculus
3	516.5	70.1	479	Q91WP5	Q91wp5 mus musculus
4	509	71.1	196	Q65ZL8	Q65zl8 mus musculus
5	506	69.7	117	HV54_MOUSE	P18525 mus musculus
6	503	69.3	117	HV55_MOUSE	P18526 mus musculus
7	497.5	68.5	119	Q920E7	Q920e7 mus musculus
8	495	68.2	117	HV59_MOUSE	P18530 mus musculus
9	486.5	67.0	480	Q91XE1	Q91xe1 mus musculus
10	483.5	66.6	470	Q6PJ44	Q6pja4 homo sapien
11	483	66.5	613	Q8WUK1	Q8wuk1 homo sapien
12	479	66.0	117	HV58_MOUSE	P18529 mus musculus
13	476	65.6	117	HV53_MOUSE	P18524 mus musculus
14	475.5	65.5	597	Q96BB9	Q96bb9 homo sapien
15	475	65.4	473	Q91Z05	Q91z05 mus musculus
16	469.5	64.7	485	Q6PDB8	Q6pdb8 mus musculus
17	467.5	64.4	464	Q6MZU6	Q6mzu6 homo sapien
18	466	64.2	475	Q6MZQ6	Q6mzq6 homo sapien
19	465.5	64.1	499	Q8N5K4	Q8n5k4 homo sapien
20	462	63.6	494	Q96K68	Q96k68 homo sapien
21	461.5	63.6	478	Q6PI81	Q6pi81 homo sapien
22	459	63.2	606	Q6GMV2	Q6gmv2 homo sapien
23	457.5	63.0	493	Q6GMX2	Q6gmx2 homo sapien
24	457	62.9	465	Q6P6C4	Q6p6c4 homo sapien
25	456	62.8	136	HV16_MOUSE	P01783 mus musculus
26	455.5	62.7	255	Q6KB05	Q6kb05 mus musculus
27	452	62.3	573	Q8WU38	Q8wu38 homo sapien
28	451	62.1	544	Q6PJ95	Q6pj95 homo sapien
29	447.5	61.6	466	Q6IN78	Q6in78 homo sapien
30	444.5	61.2	493	Q8NCL6	Q8nc16 homo sapien
31	443	61.0	117	HV3C_HUMAN	P01764 homo sapien

32	442.5	61.0	472	2	Q6N089	Q6n089 homo sapien
33	442	60.9	479	2	Q6MZV6	Q6mzv6 homo sapien
34	441	60.7	473	2	Q6MZV7	Q6mzv7 homo sapien
35	438	60.3	487	2	Q6ZVX0	Q6zvx0 homo sapien
36	432.5	59.6	470	2	Q7Z5W1	Q7z5w1 homo sapien
37	432.5	59.6	480	2	Q6N094	Q6n094 homo sapien
38	430.5	59.3	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
39	427.5	58.9	466	2	Q6N096	Q6n096 homo sapien
40	423	58.3	494	2	Q6ZM64	Q6zm64 homo sapien
41	421.5	58.1	493	2	Q68CN4	Q68cn4 homo sapien
42	419	57.7	483	2	Q6MZX9	Q6mzx9 homo sapien
43	415.5	57.2	487	2	Q80Z17	Q80z17 mus musculu
44	415	57.2	473	2	Q6P055	Q6p055 homo sapien
45	413	56.9	122	2	Q9UL84	Q9ul84 homo sapien

ALIGNMENTS

RESULT 1

Q99KA4					
ID	Q99KA4	PRELIMINARY;	PRT;	487	AA.
AC	Q99KA4;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Igh-VJ558 protein.				
GN	Name=Igh-VJ558;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Straubeberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
[2]					
RC	SEQUENCE FROM N.A.				
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;				
RA	Director MGC Project;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC004786; AAH04786.1; -.				
DR	HSSP; P01810; 2FBJ.				
DR	MGI; 96486; Igh-VJ558.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig_C1.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF07654; C1-set; 2.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.				
SQ	SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;				

```

Query Match      75.6%; Score 549; DB 2; Length 487;
Best Local Similarity 75.5%; Pred. No. 2.9e-46;
Matches 108; Conservative 14; Mismatches 17; Indels 4; Gaps 2;

QY 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKAASGFSFGNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKAASGFTFSYAMSWVRQTP 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRNAKNTLYLQMSLSKSEDTALYFCARDH 118
Db 61 EKRLWVASISDGSYTYPDNVKGRFTISRNAKNTLYLQMSLSKSEDTALYFCARDMG 120

QY 119 SHSVCWM--FATWGQGLTVTUSA 139
Db 121 GSPYGGYSRFDYWGQGLTITVSS 143

RESULT 2
Q91207 PRELIMINARY; PRT; 486 AA.
ID Q91207
AC Q91207
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; --
DR HSP; P01789; IMCP.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 486 AA; 52681 MW; 4FEF835125D8A70B CRC64;

Query Match      72.8%; Score 528.5; DB 2; Length 486;
Best Local Similarity 70.6%; Pred. No. 3.2e-44;
Matches 101; Conservative 18; Mismatches 19; Indels 5; Gaps 2;

QY 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKAASGFSFGNYGMSWVRQTS 60

```

```

Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKVVSFSTYDMSWVRQTP 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRNAKNTLYLQMSLSKSEDTALYFCARDH 120
Db 61 ERRLWVAIAITSGG-NTYYPDNVKGRTVSRDNKAKYTYLQMSLSKSEDTAMYYCVRPEI 119
QY 121 SV----GCWFATWGQGLTVTUSA 139
Db 120 PIYYSGSYFDSWGQGLTITVSS 142

RESULT 3
Q91WP5 PRELIMINARY; PRT; 479 AA.
ID Q91WP5
AC Q91WP5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; --
DR HSP; P01789; IMCP.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match      71.1%; Score 516.5; DB 2; Length 479;
Best Local Similarity 70.5%; Pred. No. 5e-43;
Matches 98; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

QY 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKAASGFSFGNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVPGGSLKLSKAASGLTFSYAMSWVRQSP 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRNAKNTLYLQMSLSKSEDTALYFCARDH 120
Db 61 EKRLWVAIAINGNGNTYSDTMKGRFTISRDNKAKSTLYLQMSLSRSEDTAFYYCVR--- 117

```


Qy 121 SVGCWFATWGGGTLTVSA 139
 Db 118 --GGYFDVWGAGTAVTSS 134

RESULT 4

ID Q65ZL8 PRELIMINARY; PRT; 196 AA.
 AC Q65ZL8;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE VH183-DS2-JH3-CHI protein (fragment).
 GN Name=VH183-DS2-JH3-CHI;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95362300; PubMed=7635518;
 RA Komori T., Sugiyama H.;
 RT exon induces truncated mu-chain production.";
 RL "An aberrant splicing using a 3' cryptic splice site within the CHI
 Immunology 85:166-170(1995).
 DR EMBL; S79401; AAB35023.2; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON TER 196
 SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 70.1%; Score 509; DB 2; Length 196;
 Best Local Similarity 82.8%; Pred. No. 9.8e-43;
 Matches 96; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVROT 60
 Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVROT 60
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRHNKNTLYLQMSLSKSEDTALYFCA 116
 Db 61 EKRLWVATISSGGSYTYPTDVKGRTISRHNKNTLYLQMSLSKSEDTALYFCA 116

RESULT 5

HV54 MOUSE
 ID HV54 MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
 DR PIR; JT0505; HVMS84.
 DR HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT DOMAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;
 Query Match 69.7%; Score 506; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 1.1e-42;
 Matches 97; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVROT 60
 Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVROT 60
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRHNKNTLYLQMSLSKSEDTALYFCA 117
 Db 61 EKRLWVATISSGGSYTYPTDVKGRTISRHNKNTLYLQMSLSKSEDTALYFCA 117
 RESULT 6
 HV55 MOUSE
 ID HV55 MOUSE STANDARD; PRT; 117 AA.
 AC P18526;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 345 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
 DR PIR; JT0502; HVMS34.
 DR HSSP; P01783; 1IGC.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT DOMAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
 Query Match 69.3%; Score 503; DB 1; Length 117;
 Best Local Similarity 81.2%; Pred. No. 2.1e-42;
 Matches 95; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG_LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
SQ	SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;
Query Match	66.6%; Score 483.5; DB 2; Length 470;
Best Local Similarity	65.7%; Pred.No. 9.7e-40;
Matches	92; Conservative 20; Mismatches 27; Indels 1; Gaps 1;
Qy	1 MNFGLSLIFLVLVNLKGVQCVELVESGGDLNMPGASLKLSCAASGFSPSYNGMSVVROTSS 60
Dy	1 MELGLSWFLVALDEGVQCEQLVESGGGLVQPGLSRLSCVCVGFTSSYMWVRQAP 60
Qy	61 DKRELWVASISTGGANTFYPDNVKGRTTISRENAKNTLYLQWSLKSSEDTALYPCARDSH 120
Dy	61 GKGLEWANVIKQDGSEKYVDYVKGRFTTSRDNAKNSLYLQMNSLRADETAVYVCARDGS 120
Qy	.121 S-VGCWFATWGQGLTVTVA 139
Dy	.121 SWTRDFPDPMGQGLTVTVSS 140
RESULT 11	
Q8WUK1	PRELIMINARY; PRT; 613 AA.
AC	Q8WUK1
CD	01-MAR-2002 (TtEMBLrel. 20, Created)
DT	01-MAR-2002 (TtEMBLrel. 20, Last sequence update)
DT	01-MAR-2004 (TrEMBrel. 26, Last annotation update)
DE	IIGHM protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606;
RN	[1]
RC	SEQUENCE FROM N.A.
RP	TISSUE=Primary B-Cells;
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altshul S.F., Zeeberg B., Bueto W.K., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RC	SEQUENCE FROM N.A.
RP	TISSUE=Primary B-Cells;
RA	Strausberg R.;
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC020420; AAH20420.1; -.
DR	PIR; F36005; F36005.
DR	PIR; G36005; G36005.


```
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DN IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR PIR; S05271; S05271.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD88CE263D9 CRC64;

Query Match 65.5%; Score 475.5; DB 2; Length 597;
Best Local Similarity 63.2%; Pred. No. 8e-39;
Matches 91; Conservative 26; Mismatches 22; Indels 5; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNSYGMWVRQTS 60
Db 1 MEFGLSWFLVAILKGVQCEVKLVESGGLVQPGSLRLSCAASGFSFSSYAMWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRENKNTLYLQMSLSKEDTALYFCARD-- 118
Db 61 KGLEWVASISGGSGTGYADSVKGRFTISRDNSRDTLYLQMSLRDTEATVYYCAKDPR 120

Qy 119 SHVGCWFAT--WGQGLTVTVSA 139
Db 121 GYSAGNTREDYWGQGLTVTVSS 144

RESULT 15
ID Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Expressed sequence AU044919.
DN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR PIR; S68213; S68213.
DR HSSP; P01783; IIGC.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 65.4%; Score 475; DB 2; Length 473;
Best Local Similarity 64.1%; Pred. No. 6.9e-39;
Matches 91; Conservative 21; Mismatches 22; Indels 8; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNSYGMWVRQTS 60
Db 1 MDSRLNLFVLILKGVQCEVKLVESGGLVQPGSLRLSCAASGFTFSDYGMHWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRENKNTLYLQMSLSKEDTALYFCARDSH 120
Db 61 EKGLWVAYISGSGTIIYADTVKGRFTISRDNAKNTLFLQMTSLRSEDATMYTCARE-- 118

Qy 121 SVGCWFAT--WGQGLTVTVSA 139
Db 119 ---LWLRRIDYWGQGLTVTVSS 137

Search completed: May 25, 2005, 15:56:07
Job time : 68.7544 secs
```

BEST AVAILABLE COPY

May 26 09:14:26 2005

CGG-1993-1993
GenCore - 2005
62.1321 Seconds
alignments)
5 Million cell updates/sec

CGG-1993-1993

OK W p-protein search, using

Run on: May 25, 2005, 15:35:...

US-10-006-773a-19.rag

Title: score: 689

Perfect: 100%

Sequence: 100%

Scoring: 100%

First 45 summaries

Search: 16Dec04:*

Genesep1980s:*

Genesep2000s:*

Genesep2001s:*

Genesep2002s:*

Genesep2003s:*

Genesep2004s:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	ID	Description
1	689	100.0	132	6	ABG74248 Mouse ant
2	669	97.1	128	8	ADI26648 Mouse ant
3	664	96.4	127	2	AAW01145 MAB 10.1
4	663	96.2	135	7	ABR82783 Hybridoma
5	663	96.2	135	7	ABR82893 Hybridoma
6	649	94.2	136	2	AAW01632 Ber-H2 he
7	643	93.3	136	4	AAW01632 Ber-H2 he
8	634	92.0	136	8	ADO47803 AF2 antib
9	623	90.4	127	3	AAW71545 Mouse AF2
10	600	87.1	121	2	AAW47085 Mouse J59
11	600	87.1	121	2	AAW90370 J591 mono
12	600	87.1	121	2	AAW90370 J591 mono
13	567	82.3	109	2	AAW36222 Murine mo
14	562	81.6	107	2	AAW47086 Mouse J59
15	562	81.6	107	2	AAW90374 J591 mono
16	562	81.6	107	2	AAW36225 Monoclonal
17	562	81.6	107	3	AAW10444 Murine mo
18	551	80.0	107	8	ADW7177 Anti-VAP-
19	534	77.5	101	5	ABB07176 Mouse 09
20	534	77.5	101	8	ADI26668 Mouse ant
21	532	77.2	133	2	AAW21934 Variable
22	532	77.2	133	2	AAW05264 Antibody
23	532	77.2	133	5	ABG98315 Murine hu
24	530	76.9	133	2	AAW21936 Variable
25	530	76.9	133	2	AAW05266 Antibody

ALIGNMENTS

RESULT 1

ABG74248

ID ABG74248 standard; protein; 132 AA.

XX AC ABG74248;

XX DT 22-APR-2003 (first entry)

XX DB Mouse antibody 3E11 light chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; light chain variable region; mouse.

XX OS Mus sp.

XX US2002132983-A1.

XX PD 19-SEP-2002.

XX PF 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PA 30-NOV-2000; 2000US-0250089P.

XX PI (JUNG/) JUNGHANS R P.

XX PT Junghans RP;

XX WPI; 2003-2089946/20.

XX N-PSDB; ABX16574.

XX DR New chimera molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 18; 35pp; English.

XX CC The invention relates to a chimeric molecule comprising the GD3 (ganglioside antigen) binding domain of antibody MB3.6, with any of 3 variable gene sequences, or the PSMA (prostate-specific membrane antigen) binding domain of antibody 3D8, 4D4 and 3E11, with variable gene sequences, the zeta signalling chain of the T cell receptor and an intervening Cdelta alpha hinge in which cysteine residues have been mutated. The chimeric molecules expressed in T cells or NK cells or other effector cells are useful in treating patients with cancers expressing

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives), and/or together with each other or with heterologous constructs to engage additional stimulatory and functional properties of the effector cells to enhance the antitumour therapeutic efficacy (claimed). They are particularly useful in disorders including melanoma, neuroendocrine tumours and prostate and small cell lung cancer. The present sequence represents the mouse antibody 3E11 light chain variable region

XX Sequence 132 AA;

Query Match 100.0%; Score 689; DB 6; Length 132;
 Best Local Similarity 100.0%; Pred. No. 6.6e-47;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVSWY 60
 DB 1 MGKMSQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVSWY 60

QY 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPY 120
 DB 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPY 120

QY 121 TFGGGTKLEIKR 132
 DB 121 TFGGGTKLEIKR 132

RESULT 2

ID AD126648 standard; protein; 128 AA.

XX AC AD126648;

XX 15-APR-2004 (first entry)

DE Mouse anti-IgM antibody light chain protein #1.

Mouse; antibody; IgM; remyelination; neuronal growth; autoantibody; demyelination disease; multiple sclerosis; central nervous system; CNS; glial cell proliferation; Theiler's murine encephalomyelitis virus infection; CNS injury; spinal cord injury.

XX PA--A1.

XX PA

XX XX

XX PT

XX XX

DR DR

DR DR

XX XX

PT PT

XX XX

PS PS

XX XX

CC CC

CC CC

Example 4; Fig 15; 159pp; English.

The invention relates to an antibody (I) produced in a human or immunocompetent host with an antibody peptide, and

ing or preventing a

tem in a human or

produced

ing the

ing the

ing the

ing the

ing the

ing the

ing the

ing the

ing the

ing the

antibody, where the peptide comprises a human anti-IgM antibody fragment given in the specification, or active fragments. Also included are stimulating remyelination of central nervous system (CNS) axons in a mammal comprising administering a monoclonal antibody, or mixtures of monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CNS, including oligodendrocytes), stimulating the proliferation of glial cells in CNS axons in a mammal (comprising administering a monoclonal antibody, or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CNS), treating or preventing a demyelinating disease of the CNS in a mammal (comprising administering a monoclonal antibody, or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CNS, and to stimulate remyelination of axons of the CNS), stimulating, in vitro, the proliferation of glial cells from mixed cell culture, stimulating remyelination of CNS axons in a mammal, a DNA sequence (or degenerate variant of it) which encodes an antibody (or a peptide analogue, hapten, or active fragment of it, where the DNA sequence consists of a sequence encoding an anti IgM antibody), a probe capable of screening for the antibody, an assay for screening drugs and other agents for the ability to modulate the production or mimic the activities of MAB sHGM22, sHGM46, or combinations of them, a recombinant virus transformed with recombinant antibody nucleic acids or vector, imaging a portion of the CNS using the antibody and diagnosing or monitoring demyelination and/or remyelination of the CNS comprising using CNS image. The antibody is used to stimulate remyelination of CNS axons, and to stimulate the proliferation of glial cells in CNS axons, optionally in vitro. The antibody is used to treat or prevent a demyelinating disease of the CNS in a human or domestic animal, such as multiple sclerosis, or a disease, other injury or dysfunction of the CNS, preferably the mammal is a mouse infected with Strain DA of Theiler's murine encephalomyelitis virus. The antibody is used to treat a spinal cord injury and used to screen drugs and other agents for the ability to modulate the production or mimic the activities of the antibody. The antibody can be used to image a portion of the CNS which can be used to diagnose or monitor demyelination and/or remyelination of the CNS. The present sequence is a variable region of a mouse anti-IgM antibody (or fragment).

SQ Sequence 128 AA;

Query Match 97.1%; Score 669; DB 8; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.4e-45;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVSWYQOKP 64

DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVSWYQOKP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124

DB 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 120

QY 125 GTKLEIKR 132

DB 121 GTKLEIKR 128

RESULT 3

ID AAW01145 standard; protein; 127 AA.

XX AC AAW01145;

XX 10-FEB-1997 (first entry)

XX MAB 10.1 light chain, directed against type II phospholipase A2.

XX Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;

XX Cerebral infarction; acute kidney failure; colitis; chronic rheumatism;

XX adult respiratory distress syndrome; cardiac shock; treatment;

XX preclinical testing, disease, hybridoma


```

XX OS Mus musculus.
XX FH Key
XX FT Binding-site
XX FT Binding-site
XX FT Binding-site
XX FT Binding-site
XX FT Binding-site
XX PN WO9620959-A1.
XX PD 11-JUL-1996.
XX XX 27-DEC-1995; 9SWO-JP002714.
XX PF 29-DEC-1994; 9AJP-00340006.
XX PR (YAMA ) YAMANOUCHI PHARM CO LTD.
XX PA Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;
XX PI WPI; 1996-333946/33.
XX DR N-PSDB; AAT40805.
XX PT Monoclonal antibody inhibiting type II phospholipase A2 activity - for
XX FT treatment of myocardial and cerebral infarction.
XX PS Claim 6; Fig 13; 69pp; Japanese.
XX CC Monoclonal antibodies which inhibit type II phospholipase A2 are useful
XX CC in the treatment of myocardial infarction, cerebral infarction, acute
XX CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult
XX CC respiratory distress syndrome and colitis. The antibodies were generated
XX CC by immunising Balb/C mice with recombinant human type II phospholipase
XX CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1
XX CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase
XX CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4
XX CC and 10.1. These were cultured and the antibody isolated from the culture
XX CC supernatant by precipitation with ammonium sulphate and purification on a
XX CC column of protein A-Sepharose CL4B. Because the antibody acts on the
XX CC primate and mouse forms of enzyme as well as human it is particularly
XX CC suitable for preclinical testing
XX SQ Sequence 127 AA;

Query Match 96.4%; Score 664; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.9e-45;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQKP 64
DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQKP 60

QY 65 EQSPKLLIYGASNYRTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 124
DB 61 EQSPKLLIYGASNYRTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 120

QY 125 GTKLEIK 131
DB 121 GTKLEIK 127

RESULT 4
ABR82783
ID ABR82783 standard; protein; 135 AA.
XX AC ABR82783;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.

XX CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-196.
XX Homo sapiens.
XX PN WO2003072036-A2.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005323.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.
XX PA (UYDU-) UNIV DUKE.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tedder T, Tuscano J;
XX DR WPI; 2003-712652/67.
XX DR N-PSDB; ACF36433.
XX PT Treating a human patient diagnosed with a B-cell malignancy by
XX FT administering a blocking anti-CD22 monoclonal antibody binding to the
XX FT first two Ig-like domains of native human CD22 (hCD22).
XX PS Claim 32; Fig 23; 72pp; English.
XX CC The invention relates to treating a human patient diagnosed with a B-cell
XX CC malignancy. The method involves (a) administering to the human patient a
XX CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like
XX CC domains, or to an epitope within the first two Ig-like domains of native
XX CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the
XX CC malignancy to the treatment. The method is useful for treating a human
XX CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,
XX CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy
XX CC cell leukemia or prolymphocytic leukemia. The present sequence represents
XX CC the amino acid sequence for kappa light chain V-J junction for anti-CD22
XX CC antibody from hybridoma HB22-196
XX SQ Sequence 135 AA;

Query Match 96.2%; Score 663; DB 7; Length 135;
Best Local Similarity 99.2%; Pred. No. 7.6e-45;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQKP 64
DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQKP 60

QY 65 EQSPKLLIYGASNYRTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 124
DB 61 EQSPKLLIYGASNYRTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 120

QY 125 GTKLEIKR 132
DB 121 GTKLEIKR 128

RESULT 5
ABR82893
ID ABR82893 standard; protein; 135 AA.
XX AC ABR82893;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
XX CD22; autoimmune disease; anti-CD22 antibody; iImmunosuppressive;
XX cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;
XX antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;
XX antidiabetic; antiallergic; gene therapy; HB22-196.

```

XX OS Homo sapiens.
 XX PN WO2003072736-A2.
 XX PD 04-SEP-2003.
 XX XX
 XX 21-FEB-2003; 2003WO-US005549.
 XX PF
 XX 21-FEB-2002; 2002US-0359419P.
 XX PR 21-OCT-2002; 2002US-0420472P.
 XX XX
 XX PA (UYDU-) UNIV DUKE.
 XX XX
 XX PI Tedder TF;
 XX XX
 XX DR WPI; 2003-721765/68.
 XX DR N-PSDB; ACF36501.
 XX XX
 XX PT Treating an autoimmune disease or a B-cell malignancy in a human patient
 XX PT comprises administering an amount of an anti-CD22 monoclonal antibody to
 XX PT the patient and monitoring the response of the disease to the treatment.
 XX XX
 XX PS Claim 4; Fig 23; 69pp; English.
 XX CC The invention relates to treating a human patient diagnosed with an
 XX CC autoimmune disease. The method involves administering to the patient an
 XX CC amount of a blocking anti-CD22 monoclonal antibody and monitoring the
 XX CC response of the autoimmune disease to the treatment. The method is useful
 XX CC in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
 XX CC erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
 XX CC Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
 XX CC allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
 XX CC present sequence represents the amino acid sequence for kappa light chain
 XX CC V-J function for anti-CD22 antibody from hybridoma HB22-196
 XX XX
 XX SQ Sequence 135 AA;
 Query Match 96.2%; Score 663; DB 7; Length 135;
 Best Local Similarity 99.2%; Pred. No. 7.6e-45;
 Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 MESQTQVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSWYQQKP 64
 Db 1 MESQTQVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSWYQQKP 60
 QY 65 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSYPYTFGG 124
 Db 61 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSYPYTFGG 120
 QY 125 GTKLEIKR 132
 Db 121 GTKLEIKR 128
 RESULT 6
 AAW01632
 ID AAW01632 standard; protein; 136 AA.
 XX AC AAW01632;
 XX XX
 XX 22-JUL-1997 (first entry)
 XX DT
 XX DE Ber-H2 heavy kappa chain.
 XX XX
 XX CD30; immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
 XX KW Ber-H2.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..29
 XX FT /label= sig_peptide

FT Protein 30..136
 FT /label= mat_protein
 XX PN DE19543039-C1.
 XX PD 21-NOV-1996.
 XX XX
 XX 08-NOV-1995; 95DE-01043039.
 XX PF
 XX 08-NOV-1995; 95DE-01043039.
 XX PR
 XX (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
 XX PA
 XX Ziegler A, Stein H;
 XX DR WPI; 1996-507017/51.
 XX DR N-PSDB; AAT58329.
 XX XX
 XX PT DNA mola. encoding CD30-specific immunoglobulin variable regions - useful
 XX PT for cancer diagnosis or therapy.
 XX XX
 XX PS Claim 15; Page 15; 20pp; German.
 XX CC The ligands are useful for diagnosis or therapy of CD30 expressing
 XX CC cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from
 XX CC cells of the mouse myeloma hybrid line Ber-H2. cDNA was isolated using
 XX CC reverse transcriptase. A VHDJ fragment contg. band was cut from a gel and
 XX CC purified. DNA corresponding to VK and Vgamma was isolated and cloned into
 XX CC vectors. Oligonucleotides used are given in AAT58331 to AAT58340
 XX XX
 XX SQ Sequence 136 AA;
 Query Match 94.2%; Score 649; DB 2; Length 136;
 Best Local Similarity 95.4%; Pred. No. 9.8e-44;
 Matches 125; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGIKMESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVTVVSWY 60
 Db 6 MGIKMESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVTVVSWY 65
 QY 61 QOKPQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSYPY 120
 Db 66 QOKPQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSYPY 125
 QY 121 TFGGGTKLEIK 131
 Db 126 TFGGGTKLEIK 136
 RESULT 7
 AAB69693
 ID AAB69693 standard; protein; 136 AA.
 XX AC AAB69693;
 XX XX
 XX 30-APR-2001 (first entry)
 XX DT
 XX XX Murine AF2 antibody light chain SEQ ID NO: 99.
 XX DE
 XX KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 XX KW light chain; graft versus host disease; transplant; autoimmune disease;
 XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 XX KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
 XX OS Mus sp.
 XX XX
 XX PN US6180370-B1.
 XX XX
 XX PD 30-JAN-2001.
 XX XX
 XX PF 07-JUN-1995; 95US-00484537.
 XX XX
 XX PR 28-DEC-1988; 88US-00290975.

```

PR 13-FEB-1989; 89US-00310252.
PR 28-SEP-1990; 90US-00590274.
PR 19-DEC-1990; 90US-00634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX N-PSDB; AAF58757.
XX
XX Producing humanized immunoglobulin, involves producing a cell containing
XX DNA segments encoding humanized heavy and light chain variable regions,
XX and expressing the DNA segments in the cell.
XX
XX Example 9; Fig 43; 145pp; English.
XX
XX The present invention describes a method of producing humanised
XX immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX humanised version of an immunoglobulin. This is obtained by comparing a
XX donor and human immunoglobulin and producing a combined antibody which
XX contains part of each. These are useful in the treatment of graft-versus-
XX host disease, transplant rejection, autoimmune diseases such as diabetes,
XX rheumatoid arthritis, myaschenia gravis, multiple sclerosis and systemic
XX lupus erythematosus, herpes infections, CMV virus infections and myeloid
XX leukaemia. The present sequence is an antibody used to demonstrate the
XX method of the invention
XX
XX Sequence 136 AA;
XX
XX Query Match 93.3%; Score 643; DB 4; Length 136;
XX Best Local Similarity 93.1%; Pred. No. 2.9e-43;
XX Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 1 MGIKMESQTLVFISILLWLYGADGNIWMTQSPKMSMSVGERVLTCKASENVVTVYSWY 60
XX Db 6 MGIKMESQTLVFISILLWLYGADGNIWMTQSPKMSMYISIGERVLTCKASENVDTYYSWY 65
XX
XX Qy 61 QQRPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGQSYYPY 120
XX Db 66 QQRPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGQSYNYPF 125
XX
XX Qy 121 TFGSGTKLEIK 131
XX Db 126 TFGSGTKLEIK 136
XX
XX RESULT 8
XX ADO47803
XX ID ADO47803. standard; protein; 136 AA.
XX
XX AC ADO47803;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE AF2 antibody light chain variable region.
XX
XX KW humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;
XX donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;
XX IL-2 receptor; T-cell mediated disorder; AF2 antibody;
XX light chain variable region.
XX
XX OS Unidentified.
XX
XX PN US2004058414-A1.
XX
XX PD 25-MAR-2004.
XX
XX PF 30-MAY-2003; 2003US-00452357.
XX
XX PR 28-DEC-1988; 88US-00290975.
XX 13-FEB-1989; 89US-00310252.
XX 28-SEP-1990; 90US-00590274.
XX

```

```

PR 07-JUN-1995; 95US-00484537.
PR 22-NOV-2000; 2000US-00718993.
XX
XX (QUEB/) QUEEN C L.
XX (COMS/) CO M S.
XX (SCHN/) SCHNEIDER W P.
XX (LAND/) LANDOLFI N F.
XX (COEL/) COELINGH K L.
XX (SELI/) SELICK H E.
XX
XX Queen CL, Co MS, Schneider WP, Landolfi NF, Coelingh KL;
XX Selick HE;
XX
XX WPI; 2004-304235/28.
XX N-PSDB; ADO47802.
XX
XX Designing humanized immunoglobulin chain comprises substituting human
XX framework amino acids of acceptor immunoglobulin with corresponding amino
XX acid from donor immunoglobulin at position in immunoglobulin.
XX
XX Disclosure; Fig 54; 130pp; English.
XX
XX The invention describes a method of designing a humanised immunoglobulin
XX (Ig) chain. The method comprises substituting human framework amino acids
XX of the acceptor Ig with a corresponding amino acid from the donor Ig at a
XX position in the Igs, where the amino acid is immediately adjacent to one
XX of the CDR's or the amino acid is predicted to have a side chain atom
XX whose Van der Waals surface is 3 angstroms from the CDR's in three-
XX dimensional Ig model and is capable of interacting with the antigen or
XX with the CDR's of the humanised Ig that when the chain is a heavy chain,
XX substituted amino acid(s) is capable of interacting with CDR's 2 or 3.
XX Also described are: an Ig comprising two light/heavy chains; a DNA
XX sequence which upon expression encodes a humanised Ig chain; a
XX polynucleotide composition comprising a DNA sequence coding for a
XX humanised Ig; a composition comprising a pure humanised immunoglobulin
XX capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL
XX -2 receptor; treating T-cell mediated disorders in a human patient
XX comprising administering to the patient a therapeutic dose of an Ig; and
XX a composition comprising a pure humanised Ig reactive with the p75 chain
XX of the human IL-2 receptor. The method is used for designing a humanised
XX immunoglobulin chain, useful for treating T-cell mediated disorders in a
XX human patient. The invented method produces an Ig chain that is easily
XX and economically produced. This is the amino acid sequence of AF2
XX antibody light chain variable region, residues of which can be replaced
XX with residues from a mouse antibody light chain variable region to create
XX a humanised antibody.
XX
XX Sequence 136 AA;
XX
XX Query Match 92.0%; Score 634; DB 8; Length 136;
XX Best Local Similarity 92.4%; Pred. No. 1.5e-42;
XX Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
XX
XX Qy 1 MGIKMESQTLVFISILLWLYGADGNIWMTQSPKMSMSVGERVLTCKASENVVTVYSWY 60
XX Db 6 MGIKMESQTLVFISILLWLYGADGNIWMTQSPKMSMYISIGERVLTCKASENVDTYYSWY 65
XX
XX Qy 61 QQRPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGQSYYPY 120
XX Db 66 QQRPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGQSYNYPF 125
XX
XX Qy 121 TFGSGTKLEIK 131
XX Db 126 TFGSGTKLEIK 136
XX
XX RESULT 9
XX AAY71545
XX ID AAY71545 standard; protein; 127 AA.
XX
XX AC AAY71545;
XX
XX DT 12-OCT-2000 (first entry)

```

XX Mouse AF2 antibody light chain variable region (AF2-VL).

DE Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL;

XX light chain variable region; VL; heavy chain variable region; VH; Igg2b;

XX gamma-interferon; IFN; complementarity determining region; CDR; FR;

XX framework region; immunosuppressive; antiinflammatory; antisclerotic;

XX gastrointestinal; antidiabetic; antiarthritic; dermatological; inhibitor;

XX autoimmune disease; graft versus host disease; organ transplant;

XX multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;

XX systemic lupus erythematosus; SLE; Crohn's disease.

XX Mus sp.

XX OS

XX Location/Qualifiers

XX Key

XX Peptide

XX 1..20 /note= "N-terminal peptide"

XX Protein

XX 21..127 /note= "Mature mouse antibody AF2 light chain variable

XX region (AF2-VL)"

XX 44..54 /label= CDR

XX /note= "Complementarity determining region"

XX 70..76 /label= CDR

XX /note= "Complementarity determining region"

XX 109..117 /label= CDR

XX /note= "Complementarity determining region"

XX WO200032634-A1.

XX PN

XX PD

XX 08-JUN-2000.

XX PF

XX 29-NOV-1999; 99WO-US028195.

XX PR

XX 01-DEC-1998; 98US-0110523P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;

XX WPI; 2000-412292/35.

XX N-PSDB; AAD01345.

XX Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-

XX interferon for the treatment of autoimmune diseases, e.g. multiple

XX sclerosis and diabetes.

XX Claim 1; Fig 1A; 32pp; English.

XX The present amino acid sequence is the mouse AF2 antibody, light chain

XX variable region (AF2-VL). It has Igg2b isotype and kappa light chain. It

XX is used for the construction of humanised version of mouse AF2 antibody

XX HuZAF, that comprises mouse antibody AF2 complementarity determining

XX regions (CDRs) functionally joined to the human acceptor antibody EU

XX framework region (FR). HuZAF antibody specifically binds to and

XX neutralises gamma-interferon (IFN). They can also block the binding of

XX mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences

XX that are immunogenically active in humans and remains unaffected by

XX immune responses, that may reduce its activity or circulating half-life.

XX HuZAF may be administered to treat autoimmune diseases such as graft

XX versus host disease following organ transplant, Type I diabetes, multiple

XX sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus

XX (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and

XX inflammatory bowel disease like, Crohn's disease

XX Sequence 127 AA;

SQ

Query Match 90.4%; Score 623; DB 3; Length 127;

Best Local Similarity 92.9%; Pred. No. 1e-41;

Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSYGERVTLTKASENVTVVSWYQKP 64

DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMVVSIGERVTLTKASENVTVVSWYQKP 60

QY 65 EQSPKLLIYGASNRVTGVPDRPTGSGSATDFTLTSSVOAEDLADYHCCQGSYPYTFGG 124

DB 61 EQSPKLLIYGASNRVTGVPDRPTGSGSATDFTLTSSVOAEDLADYHCCQGSYPYTFGS 120

QY 125 GTKLEIK 131

DB 121 GTKLEIK 127

RESULT 10

AAW47085

ID AAW47085 standard; protein; 121 AA.

XX AC AAW47085;

XX 26-JUN-1998 (first entry)

XX DE Mouse J591 monoclonal antibody light chain.

XX KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;

XX cancer; vascular endothelial cell; metastatic adenocarcinoma.

XX OS Mus sp.

XX WO9803873-A1.

XX 29-JAN-1998.

XX 17-JUL-1997; 97WO-US012035.

XX 18-JUL-1996; 96US-0022125P.

XX 09-APR-1997; 97US-00838682.

XX (CORR) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 1998-120937/11.

XX N-PSDB; AAV13951.

XX Destroying cancer cells with agent that binds to prostate specific

XX membrane antigen - on vascular endothelial cells near the cancer, or on

XX normal, hypertrophic or cancerous prostatic cells, also used for

XX diagnosis.

XX Example 12; Page 57; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody light

XX chain from an example of the present invention. The present invention

XX describes the elimination of cancer cells by treating vascular

XX endothelial cells (VEC) close to the cancer with an agent (A) able to

XX bind to the extracellular domain (ECD) of prostate specific membrane

XX antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.

XX Also described are: (1) the detection of cancer tissue by detecting

XX binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)

XX eliminating or detecting normal, benignly hyperplastic or cancerous

XX prostate epithelial cells using optionally labelled (A); (3) hybridomas

XX that produce a monoclonal antibody (Mab) that binds to PSMA. The method

XX is used to treat renal, urothelial, colon, lung, rectal or breast cancers

XX and metastatic adenocarcinoma of the liver. The diagnostic method is

XX particularly used to detect recurrence of prostatic disease or to monitor

XX the effect of treatments for prostate cancer (presence of PSMA in the

XX serum indicates that prostate cells are being lysed). (A) binds to an

XX epitope of PSMA expressed on live cells (contrast antibody 7E11 which

XX only binds after cell lysis), allowing targeting of live, unfixed cells

XX and thus providing more efficient treatment and diagnosis. Both cancer

XX cells themselves and the VEC on which they depend are killed. All VEC

XX close to cancer cells express PSMA, whatever the type of cancer, but

XX normal VEC do not

```

XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTITSSVQAEADLADYHCGQGSYPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTITSSVQAEADLADYHCGQGSYPYTFGGGTKLEIKR 114

RESULT 11
AAY90370
ID AAY90370 standard; protein; 121 AA.
XX AC AAY90370;
XX DT 15-JAN-2001 (first entry)
XX DE J591 monoclonal antibody kappa light chain protein sequence #1.
XX KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
XX KW prostate specific membrane antigen; prostate cancer; kappa light chain.
XX OS Homo sapiens.
XX FN US6107090-A.
XX PD 22-AUG-2000.
XX PF 09-APR-1997; 97US-00838682.
XX PR 06-MAY-1996; 96US-0016976P.
XX PR 18-JUL-1996; 96US-0022125P.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Bander NH;
XX WPI; 1998-120937/11.
XX DR N-PSDB; AAA37832.
XX PT Destroying cancer cells with agent that binds to prostate specific
PT membrane antigen - on vascular endothelial cells near the cancer, or on
PT normal, hypertrophic or cancerous prostatic cells, also used for
PT diagnosis.
XX PS Example 12; Fig 10; 33pp; English.
XX CC This sequence is the kappa light chain of the monoclonal antibody J591.
CC The invention relates to an isolated antibody or its antigen binding
CC portion (I) which binds to an extracellular domain of prostate specific
CC membrane antigen and which does not require cell lysis to bind to the
CC extracellular domain. The antibody or its antigen binding portion is
CC selected for its ability to bind to live cells. (I) is useful for
CC diagnosis of diseases associated with the presence of normal, benign
CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
CC used for identifying the recurrence of such diseases, particularly when
CC the disease is localised in a particular biological material of the
CC patient for e.g. recurrence of prostatic disease. They can also be used
CC alone or bound to a substance effective to kill cancerous prostate
CC epithelial cells as a therapy for prostate cancer. Binding and
CC internalising of the antibody with the prostate specific membrane
CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
CC agents. (I) targets only prostate epithelial cells and other tissue are
CC spared which provides safer treatment particularly for elderly patients.
CC The antibodies bind to living prostate cells and treatments using these
CC antibodies are more effective than those which target lysed prostate

```

```

CC cells
XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTITSSVQAEADLADYHCGQGSYPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTITSSVQAEADLADYHCGQGSYPYTFGGGTKLEIKR 114

RESULT 12
AAB36222
ID AAB36222 standard; protein; 121 AA.
XX AC AAB36222;
XX DT 15-FEB-2001 (first entry)
XX DE Murine monoclonal antibody J591 kappa light chain #1.
XX KW Mouse; antibody; heavy chain; prostate cancer; biological agent.
XX OS Mus sp.
XX FN US6136311-A.
XX PD 24-OCT-2000.
XX PF 17-JUL-1997; 97US-00895914.
XX PR 06-MAY-1996; 96US-0016976P.
XX PR 18-JUL-1996; 96US-0022125P.
XX PR 09-APR-1997; 97US-00838682.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Bander NH;
XX WPI; 1998-120937/11.
XX DR N-PSDB; AAC66542.
XX PT Destroying cancer cells with agent that binds to prostate specific
PT membrane antigen - on vascular endothelial cells near the cancer, or on
PT normal, hypertrophic or cancerous prostatic cells, also used for
PT diagnosis.
XX PS Example 12; Fig 10; 35pp; English.
XX CC The present invention describes a method of killing cancer cells,
CC particularly prostate cancer cells, by directing a biological agent to
CC the cells which then binds to a prostate specific membrane antigen and
CC causes the molecule to be internalised. The internalisation of the agent,
CC which may be bound to a drug or which may act to kill the cell alone,
CC then leads to the death of the cell. The present sequence forms part of
CC an antibody which may be used as the biological agent of the invention.
CC In addition to prostate cancer, the method can be used with renal,
CC urothelial, colon, renal, lung and breast cancer cells, and cancerous
CC cells of metastatic adenocarcinoma to the liver
XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78

```

Db 1 LYGADGNVMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNR 60
 QY 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 132
 Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 114

RESULT 13
 AAR27144
 ID AAR27144 standard; protein; 109 AA.
 XX
 AC AAR27144;
 XX
 DT 09-SEP-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1998 (first entry)
 XX
 DE 1E6 kappa light chain variable region.
 XX
 KW Chimeric; heavy chain; variable region; monoclonal antibody;
 KW lymphocyte function associated antigen-3; LFA-3; inflammation;
 KW autoimmune disease; immunomodulation; systemic lupus erythematosus;
 KW rheumatoid arthritis; thyroiditis.
 XX
 OS Homo sapiens.
 OS Unidentified.
 XX

Key Location/Qualifiers
 FH Domain 24..34
 FT /note= "CDR1"
 FT Domain 50..56
 FT /note= "CDR2"
 FT Domain 89..97
 FT /note= "CDR3"
 XX
 EP503646-A1.
 XX
 PD 16-SEP-1992.
 XX
 PF 12-MAR-1992; 92EP-00104318.
 XX
 PR 12-MAR-1991; 91US-00667975.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Sato VL, Chisholm PL, Wallner BP;
 XX
 DR WPI; 1992-309758/38.
 DR N-PSDB; AAQ28653.
 XX
 XX Monoclonal antibodies active against lymphocyte function associated
 PT antigen-3 - for treating inflammation and autoimmune diseases, and for
 PT detecting LFA-3 protein in a sample.
 XX
 PS Claim 19; Page 14; 30pp; English.
 XX
 CC Light and heavy chain variable region sequences were deduced from the DNA
 CC sequences obt'd. by PCR of DNA sequences obt'd. from the hybridoma cell
 CC line 1E6-2C12 (ATCC HB 10693). The light and heavy chain regions may be
 CC used to construct a monoclonal antibody active against LFA-3 which blocks
 CC adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be
 CC used in the treatment and diagnosis of acute and chronic inflammation,
 CC autoimmune diseases and for immuno- modulation including systemic lupus
 CC erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to feature Table Key
 XX
 SQ Sequence 109 AA;

Query Match 82.3%; Score 567; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.3e-37;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 NTWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 84
 Db 1 NTWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60
 QY 85 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 132
 Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 108

RESULT 14
 AAW47086
 ID AAW47086 standard; protein; 107 AA.
 XX
 AC AAW47086;
 XX
 DT 26-JUN-1998 (first entry)
 XX
 DE Mouse J591 monoclonal antibody light chain variable region.
 XX
 KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
 KW cancer; vascular endothelial cell; metastatic adenocarcinoma.
 XX
 OS Mus sp.
 XX
 PN WO9803873-A1.
 XX
 PD 29-JAN-1998.
 XX
 PF 17-JUL-1997; 97WO-US012035.
 XX
 PR 18-JUL-1996; 96US-0022125P.
 PR 09-APR-1997; 97US-00838682.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Bander NH;
 XX
 DR WPI; 1998-120937/11.
 DR N-PSDB; AAV13952.
 XX
 PT Destroying cancer cells with agent that binds to prostate specific
 PT membrane antigen - on vascular endothelial cells near the cancer, or on
 PT normal, hypertrophic or cancerous prostatic cells, also used for
 PT diagnosis.
 XX
 PS Example 12; Page 60; 94pp; English.
 XX
 CC The present sequence represents the mouse J591 monoclonal antibody light
 CC chain variable region from an example of the present invention. The
 CC present invention describes the elimination of cancer cells by treating
 CC vascular endothelial cells (VEC) close to the cancer with an agent (A)
 CC able to bind to the extracellular domain (ECD) of prostate specific
 CC membrane antigen (PSMA). (A) both binds to the VEC and destroys the
 CC cancer cells. Also described are: (1) the detection of cancer tissue by
 CC detecting binding of labelled (A) to VEC close to, or within, a cancer
 CC tissue; (2) eliminating or detecting normal, benignly hyperplastic or
 CC cancerous prostate epithelial cells using optionally labelled (A); (3)
 CC hybridomas that produce a monoclonal antibody (MAB) that binds to PSMA.
 CC The method is used to treat renal, urothelial, colon, lung, rectal or
 CC breast cancers and metastatic adenocarcinoma of the liver. The diagnostic
 CC method is particularly used to detect recurrence of prostatic disease or
 CC to monitor the effect of treatments for prostate cancer (presence of PSMA
 CC in the serum indicates that prostate cells are being lysed). (A) binds to
 CC an epitope of PSMA expressed on live cells (contrast antibody 7E11 which
 CC only binds after cell lysis), allowing targeting of live, unfixed cells
 CC and thus providing more efficient treatment and diagnosis. Both cancer
 CC cells themselves and the VEC on which they depend are killed. All VEC
 CC close to cancer cells express PSMA, whatever the type of cancer, but
 CC normal VEC do not
 XX
 SQ Sequence 107 AA;

Query Match 81.6%; Score 562; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.7e-37;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 25 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 84
 Db 1 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
 Qy 85 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTGLEIK 131
 Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTGLEIK 107

RESULT 15

AAAY90374
 ID AAAY90374 standard; protein; 107 AA.
 AC AAAY90374;
 DT 15-JAN-2001 (first entry)
 DE J591 monoclonal antibody light chain protein sequence fragment.
 KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
 KW prostate specific membrane antigen; prostate cancer; light chain.
 OS Homo sapiens.
 PN US6107090-A.
 PD 22-AUG-2000.
 PF 09-APR-1997; 97US-00838682.
 PR 06-MAY-1996; 96US-0016976P.
 PR 18-JUL-1996; 96US-0022125P.
 PA (CORR) CORNELL RES FOUND INC.
 PI Bander NH;
 DR WPI; 1998-120937/11.
 DR N-PSDB; AAA37834.
 PT Destroying cancer cells with agent that binds to prostate specific
 PT membrane antigen - on vascular endothelial cells near the cancer, or on
 PT normal, hypertrophic or cancerous prostatic cells, also used for
 PT diagnosis.

Example 12; Col 22; 33pp; English.

This sequence is a fragment of the light chain of the monoclonal antibody
 J591. The invention relates to an isolated antibody or its antigen
 binding portion (I) which binds to an extracellular domain of prostate
 specific membrane antigen and which does not require cell lysis to bind
 to the extracellular domain. The antibody or its antigen binding portion
 is selected for its ability to bind to live cells. (I) is useful for
 diagnosis of diseases associated with the presence of normal, benign
 hyperplastic, and cancerous epithelial cells or portions. Also it can be
 used for identifying the recurrence of such diseases, particularly when
 the disease is localised in a particular biological material of the
 patient for e.g. recurrence of prostatic disease. They can also be used
 alone or bound to a substance effective to kill cancerous prostate
 epithelial cells as a therapy for prostate cancer. Binding and
 internalising of the antibody with the prostate specific membrane
 antigen, permits the therapeutic use of intracellularly acting cytotoxic
 agents. (I) targets only prostate epithelial cells and other tissue are
 spared which provides safer treatment particularly for elderly patients.
 The antibodies bind to living prostate cells and treatments using these
 antibodies are more effective than those which target lysed prostate
 cells

CC

SQ Sequence 107 AA;

Query Match 81.6%; Score 562; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.7e-37;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 25 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 84
 Db 1 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
 Qy 85 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTGLEIK 131
 Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGGTGLEIK 107

Search completed: May 25, 2005, 15:47:24
 Job time : 64.1321 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 689

Sequence: 1 MGIMNESQTLVFISILLWLY.....GGQSYSPYTFGGGTYKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*

5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pap.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643	93.3	136	1	US-07-634-278-99
2	643	93.3	136	1	US-08-477-728-99
3	643	93.3	136	1	US-08-474-040-99
4	643	93.3	136	1	US-08-487-200-99
5	643	93.3	136	3	US-08-484-537-99
6	623	90.4	127	3	US-09-450-520A-2
7	600	87.1	121	3	US-08-838-682-11
8	600	87.1	121	3	US-08-895-914-11
9	600	87.1	121	3	US-09-357-710A-11
10	600	87.1	121	4	US-09-357-707-11
11	600	87.1	121	4	US-09-357-708-11
12	567	82.3	109	5	PCT-US92-02044-2
13	562	81.6	107	3	US-08-838-682-16
14	562	81.6	107	3	US-08-895-914-16
15	562	81.6	107	3	US-09-357-710A-16
16	562	81.6	107	4	US-09-357-707-16
17	562	81.6	107	4	US-09-357-708-16
18	523	75.9	132	1	US-08-253-877C-55
19	523	75.9	132	2	US-08-452-164A-55
20	523	75.9	132	3	US-08-976-183A-36
21	518	75.2	132	3	US-08-976-183A-37
22	505	73.3	147	2	US-08-653-402B-4
23	503	73.0	131	4	US-09-269-921-104
24	495.5	71.9	132	2	US-08-602-725-38
25	493	71.6	128	3	US-09-450-520A-6
26	487	70.7	131	1	US-08-202-047-5
27	487	70.7	131	3	US-08-964-690-5

28	477	69.2	131	2	US-08-822-028-14	Sequence 14, Appl
29	477	69.2	131	3	US-08-479-285-14	Sequence 14, Appl
30	477	69.2	131	4	US-09-503-653A-14	Sequence 14, Appl
31	476	69.1	127	3	US-08-525-539A-65	Sequence 65, Appl
32	475	68.9	154	3	US-08-513-968-36	Sequence 36, Appl
33	473	68.7	127	3	US-08-646-265A-27	Sequence 27, Appl
34	457	66.3	127	3	US-08-525-539A-49	Sequence 49, Appl
35	454	65.9	107	3	US-08-554-840-4	Sequence 4, Appl
36	454	65.9	107	4	US-08-925-339-4	Sequence 4, Appl
37	454	65.9	107	4	US-09-332-595-4	Sequence 4, Appl
38	453	65.7	133	3	US-08-579-378A-2	Sequence 2, Appl
39	453	65.7	133	5	PCT-US93-11612-2	Sequence 2, Appl
40	452	65.6	134	4	US-08-961-309-58	Sequence 58, Appl
41	449	65.2	107	3	US-08-554-840-2	Sequence 2, Appl
42	449	65.2	107	4	US-08-925-339-2	Sequence 2, Appl
43	449	65.2	107	4	US-09-332-595-2	Sequence 2, Appl
44	448	65.0	126	2	US-08-822-028-28	Sequence 28, Appl
45	448	65.0	126	3	US-08-479-285-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-99
; Sequence 99, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
 US-07-634-278-99

Query Match 93.3%; Score 643; DB 1; Length 136;
 Best Local Similarity 93.1%; Pred. No. 2.2e-57;
 Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTYSWY 60
 |||||
 Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSIGERVTLTKASENVDTYSWY 65
 |||||

QY 61 QQRPEQSPKLLIYGASNRRTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPY 120
 |||||
 Db 66 QQRPEQSPKLLIYGASNRRTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 125
 |||||

QY 121 TFGGGTKLEIK 131
 |||||
 Db 126 TFGGGTKLEIK 136
 |||||

RESULT 2
 US-08-477-728-99
 ; Sequence 99, Application US/08477728
 ; Patent No. 5585089
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,728
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 99:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 136 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-477-728-99

Query Match 93.3%; Score 643; DB 1; Length 136;
 Best Local Similarity 93.1%; Pred. No. 2.2e-57;
 Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTYSWY 60
 |||||
 Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSIGERVTLTKASENVDTYSWY 65
 |||||

QY 61 QQRPEQSPKLLIYGASNRRTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPY 120
 |||||
 Db 66 QQRPEQSPKLLIYGASNRRTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 125
 |||||

QY 121 TFGGGTKLEIK 131
 |||||
 Db 126 TFGGGTKLEIK 136
 |||||

RESULT 3
 US-08-474-040-99
 ; Sequence 99, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas P.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,040
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 99:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 136 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-474-040-99

Query Match 93.3%; Score 643; DB 1; Length 136;

Best Local Similarity 93.1%; Pred. No. 2.2e-57;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 60
Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYVIGRVTLSCKASENVVTVSWY 65

Qy 61 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
Db 66 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125

Qy 121 TFGGQTKLEIK 131
Db 126 TFGSGTKLEIK 136

RESULT 4
US-08-487-200-99
; Sequence 99, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-200-99

Query Match 93.3%; Score 643; DB 1; Length 136;

Best Local Similarity 93.1%; Pred. No. 2.2e-57;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 60
Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYVIGRVTLSCKASENVVTVSWY 65

Qy 61 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
Db 66 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125

Qy 121 TFGGQTKLEIK 131
Db 126 TFGSGTKLEIK 136

RESULT 5
US-08-484-537-99
; Sequence 99, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO. Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-537-99

Query Match 93.3%; Score 643; DB 3; Length 136;
Best Local Similarity 93.1%; Pred. No. 2.2e-57;

Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWY 60
|||||
Db 6 MGKMSQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWY 65
|||||

QY 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 120
|||||
Db 66 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYNYPF 125
|||||

QY 121 TFGGKLEIK 131
|||||
Db 126 TFGGKLEIK 136
|||||

RESULT 6
US-09-450-520A-2
; Sequence 2, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; TITLE OF INVENTION: Protein Design Labs, Inc.
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/450,520A
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/110,523
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: AF2 VL
US-09-450-520A-2

Query Match 90.4%; Score 623; DB 3; Length 127;
Best Local Similarity 92.9%; Pred. No. 2.1e-55;
Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 MESQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWYQKP 64
|||||
Db 1 MESQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWYQKP 60
|||||

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGG 124
|||||
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYNYPF 120
|||||

QY 125 GTKLEIK 131
|||||
Db 121 GTKLEIK 127
|||||

RESULT 7
US-08-838-682-11
; Sequence 11, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.

ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,682
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-682-11

Query Match 87.1%; Score 600; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWYQKPQSPKLLIYGASNR 78
|||||
Db 1 LYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVTVVSWYQKPQSPKLLIYGASNR 60
|||||

QY 79 YTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTKLEIKR 132
|||||
Db 61 YTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTKLEIKR 114
|||||

RESULT 8
US-08-895-914-11
; Sequence 11, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,914
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/016,976
FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-895-914-11

Query Match      87.1%; Score 600; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 9
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1997-04-09
; PRIOR FILING DATE: 1997-04-09
; PRIOR FILING DATE: 1996-05-06
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-11

Query Match      87.1%; Score 600; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 10
US-09-357-707-11
```

```
; Sequence 11, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357,707
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1997-07-17
; PRIOR FILING DATE: 1997-07-17
; PRIOR FILING DATE: 1996-05-06
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-11

Query Match      87.1%; Score 600; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 11
US-09-357-708-11
; Sequence 11, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1997-07-17
; PRIOR FILING DATE: 1997-04-09
; PRIOR FILING DATE: 1997-04-09
; PRIOR FILING DATE: 1996-05-06
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-11

Query Match      87.1%; Score 600; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114
```

Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEDLADYHCGGYSYPYTFGGGKLEIKR 114

RESULT 12

PCT-US92-02044-2
; Sequence 2, Application PC/TUS9202044
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: SATO, Vicki L.
; APPLICANT: CHISHOLM, Patricia L.
; APPLICANT: WALLNER, Barbara P.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
; TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02044
; FILING DATE: 19920312
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,975
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B150CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0600
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02044-2

Query Match 82.3%; Score 567; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 7.7e-50; Mismatches 0; Indels 0; Gaps 0;
Matches 108; Conservative 0;
QY 25 NIVMTQSPKMSMSGVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84
Db 1 NIVMTQSPKMSMSGVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTSSVQAEDLADYHCGGYSYPYTFGGGKLEIKR 132
Db 61 RFTGSGSATDFTLTSSVQAEDLADYHCGGYSYPYTFGGGKLEIKR 108

RESULT 13

US-08-838-682-16
; Sequence 16, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-16
Query Match 81.6%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4e-49; Mismatches 0; Indels 0; Gaps 0;
Matches 107; Conservative 0;
QY 25 NIVMTQSPKMSMSGVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84
Db 1 NIVMTQSPKMSMSGVGERVTLTKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTSSVQAEDLADYHCGGYSYPYTFGGGKLEIK 131
Db 61 RFTGSGSATDFTLTSSVQAEDLADYHCGGYSYPYTFGGGKLEIK 107

RESULT 14

US-08-895-914-16
; Sequence 16, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/016,976
;; FILING DATE: 06-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/022,125
;; FILING DATE: 18-JUL-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/838,682
;; FILING DATE: 09-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldman, Michael L.
;; REGISTRATION NUMBER: 30,727
;; REFERENCE/DOCKET NUMBER: 19603/1173
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1304
;; TELEFAX: (716) 263-1600
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-895-914-16

Query Match 81.6%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 84
Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 131
Db 61 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 107

RESULT 15
US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-16

Query Match 81.6%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.4e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 84
Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 131
Db 61 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 107

Search completed: May 25, 2005, 15:58:28
Job time : 17.454 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 689

Sequence: 1 MGIMESQTLVFISILLWLX.....GGQSYPTFGGKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	100.0	132	13	US-10-006-773-19
2	669	97.1	128	14	US-10-010-729-70
3	663	96.2	135	15	US-10-372-481-31
4	663	96.2	135	15	US-10-371-797-31
5	661	95.9	128	8	US-08-779-784-34
6	634	92.0	136	15	US-10-452-357-99
7	627	91.0	136	15	US-10-389-155-84
8	627	91.0	136	15	US-10-389-417-84
9	623	90.4	127	9	US-09-992-524-2
10	600	87.1	121	10	US-09-929-665-11
11	600	87.1	121	10	US-09-929-546-11
12	562	81.6	107	10	US-09-929-665-16
13	562	81.6	107	10	US-09-929-546-16

14	534	77.5	101	14	US-10-010-729-21	Sequence 21, Appl
15	532	77.2	133	10	US-09-874-141-47	Sequence 47, Appl
16	530	76.9	133	10	US-09-874-141-51	Sequence 51, Appl
17	527	76.5	133	10	US-09-874-141-45	Sequence 45, Appl
18	512	74.3	145	15	US-10-226-795-17	Sequence 17, Appl
19	511	74.2	132	15	US-10-365-123-53	Sequence 53, Appl
20	503	73.0	107	14	US-10-160-506-48	Sequence 48, Appl
21	503	73.0	107	16	US-10-449-379-48	Sequence 48, Appl
22	503	73.0	107	16	US-10-688-015-48	Sequence 48, Appl
23	503	73.0	131	10	US-09-269-921-104	Sequence 104, Appl
24	503	73.0	131	10	US-09-509-098-2	Sequence 2, Appl
25	503	73.0	131	14	US-10-218-253-104	Sequence 104, Appl
26	493	71.6	128	9	US-09-992-524-6	Sequence 6, Appl
27	493	71.6	128	15	US-10-440-202-1	Sequence 1, Appl
28	490	71.1	107	14	US-10-160-506-64	Sequence 64, Appl
29	490	71.1	107	14	US-10-160-506-65	Sequence 65, Appl
30	490	71.1	107	16	US-10-449-379-64	Sequence 64, Appl
31	490	71.1	107	16	US-10-449-379-65	Sequence 65, Appl
32	490	71.1	107	16	US-10-688-015-64	Sequence 64, Appl
33	490	71.1	107	16	US-10-688-015-65	Sequence 65, Appl
34	487	70.7	107	14	US-10-160-506-66	Sequence 66, Appl
35	487	70.7	107	16	US-10-449-379-66	Sequence 66, Appl
36	487	70.7	107	16	US-10-688-015-66	Sequence 66, Appl
37	485	70.4	107	14	US-10-160-506-63	Sequence 63, Appl
38	485	70.4	107	16	US-10-449-379-63	Sequence 63, Appl
39	485	70.4	107	16	US-10-688-015-63	Sequence 63, Appl
40	484	70.2	107	14	US-10-160-506-50	Sequence 50, Appl
41	484	70.2	107	14	US-10-160-506-67	Sequence 67, Appl
42	484	70.2	107	14	US-10-160-506-68	Sequence 68, Appl
43	484	70.2	107	16	US-10-449-379-50	Sequence 50, Appl
44	484	70.2	107	16	US-10-449-379-67	Sequence 67, Appl
45	484	70.2	107	16	US-10-449-379-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-10-006-773-19
; Sequence 19, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-19

Query Match 100.0%; Score 689; DB 13; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.2e-56;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGIMESQTLVFISILLWLXGADGNI	VMTQSPKMSMSVGERVLT	TKCASENVTYYSWY	60
Db	1	MGIMESQTLVFISILLWLXGADGNI	VMTQSPKMSMSVGERVLT	TKCASENVTYYSWY	60
Qy	61	QQRPEQSKLLIYGASNRYTGVDP	FTGSGSATDFTT	TISSVQAEADLADYHCGGYSYPY	120
Db	61	QQRPEQSKLLIYGASNRYTGVDP	FTGSGSATDFTT	TISSVQAEADLADYHCGGYSYPY	120
Qy	121	TFGGGKLEIKR	132		
Db	121	TFGGGKLEIKR	132		

RESULT 2
US-10-010-729-70
; Sequence 70, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70

Query Match 97.1%; Score 669; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.9e-54;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 60
QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 120
QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128

RESULT 3
US-10-372-481-31
; Sequence 31, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-372-481-31
Query Match 96.2%; Score 663; DB 15; Length 135;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 60
QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 120
QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128

RESULT 4
US-10-371-797-31
; Sequence 31, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-31

Query Match 96.2%; Score 663; DB 15; Length 135;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMSSVGERVTLTKKASENVVTVSVYQKP 60
QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCGGYSYPYTFGG 120
QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128

RESULT 5
US-08-779-784-34
; Sequence 34, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION NUMBER: US/08/779,784
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
;
; US-08-779-784-34
;
; Query Match 95.9%; Score 661; DB 8; Length 128;
; Best Local Similarity 99.2%; Pred. No. 1.6e-53;
; Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 5 MESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWYQOKP 64
; Db 1 MESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWYQOKP 60
;
; Qy 65 EQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGG 124
; Db 61 EQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFRG 120
;
; Qy 125 GTKLEIKR 132
; Db 121 GTKLEIKR 128
;
; RESULT 6
; US-10-452-357-99
; Sequence 99, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William
; APPLICANT: Landolfi, Nicholas
; APPLICANT: Coelingh, Kathleen
; APPLICANT: Selick, Harold
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; FILE REFERENCE: 05882.0078.CNUS01
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION NUMBER: US/10/452,357
; APPLICATION NUMBER: US/10/452,357
; FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/718,993
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/487,200
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/634,278
; PRIOR FILING DATE: 1990-12-19
; PRIOR APPLICATION NUMBER: 07/590,275
; PRIOR FILING DATE: 1990-09-28
; PRIOR APPLICATION NUMBER: 07/310,252
; PRIOR FILING DATE: 1989-02-13
; PRIOR APPLICATION NUMBER: 07/290,975
; PRIOR FILING DATE: 1988-12-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 99
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: AF2 light chain antibody
; US-10-452-357-99
;
; Query Match 92.0%; Score 634; DB 15; Length 136;
; Best Local Similarity 92.4%; Pred. No. 5.4e-51;
; Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 1 MGKMWESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWY 60
; Db 6 MGKMWESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWY 65
;
; Qy 61 QOKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
; Db 66 QOKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125
;
; Qy 121 TFGSGTKLEIK 131
; Db 126 TFGSGTKLEIK 136
;
; RESULT 7
; US-10-389-155-84
; Sequence 84, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coelingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
```

;
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-155-84

Query Match 91.0%; Score 627; DB 15; Length 136;
Best Local Similarity 91.6%; Pred. No. 2.4e-50;
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGKIKESQTLVFISILLWLYGADGNIVMTQSPKSMYSVGERVTLTCKASENVTVVSWY 60
Db 6 MGKIKESQTLVFISILLWLYGAGNIVMTQSPKSMYSVIGERVTLSCASENVDTVSWY 65

QY 61 QOKPEQSPKLLIYGASNRYTGPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120
Db 66 QOKPEQSPKLLIYGASNRYTGVHDFRTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 125

QY 121 TFGGGTKLEIK 131
Db 126 TFGSGTKLEIK 136

RESULT 8
US-10-389-417-84
; Sequence 84, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coeligh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,417
; FILING DATE: 13-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000

;
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-417-84

Query Match 91.0%; Score 627; DB 15; Length 136;
Best Local Similarity 91.6%; Pred. No. 2.4e-50;
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGKIKESQTLVFISILLWLYGADGNIVMTQSPKSMYSVGERVTLTCKASENVTVVSWY 60
Db 6 MGKIKESQTLVFISILLWLYGAGNIVMTQSPKSMYSVIGERVTLSCASENVDTVSWY 65

QY 61 QOKPEQSPKLLIYGASNRYTGPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120
Db 66 QOKPEQSPKLLIYGASNRYTGVHDFRTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 125

QY 121 TFGGGTKLEIK 131
Db 126 TFGSGTKLEIK 136

RESULT 9
US-09-992-524-2
; Sequence 2, Application US/09992524
; Patent No. US20020091240A1
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/992,524
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/450,520
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: AF2 VL
US-09-992-524-2

Query Match 90.4%; Score 623; DB 9; Length 127;
Best Local Similarity 92.9%; Pred. No. 5.2e-50;
Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 5 MESQTLVFISILLMLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKP 64
Db 1 MESQTLVFISILLMLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKP 60
Qy 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 120
Qy 125 GTKLEIK 131
Db 121 GTKLEIK 127

RESULT 10

US-09-929-665-11
; Sequence 11, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-11

Query Match 87.1%; Score 600; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 60
Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 11

US-09-929-546-11
; Sequence 11, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-11

Query Match 87.1%; Score 600; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 60
Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 12

US-09-929-665-16
; Sequence 16, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-16

Query Match 81.6%; Score 562; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNRVTGVPD 84
Db 1 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNRVTGVPD 60

Qy 85 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIK 131
Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIK 107

RESULT 13

US-09-929-546-16
; Sequence 16, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976

; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-16

Query Match 81.6%; Score 562; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 NIWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84
Db |||||||
1 NIWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGGKLEIK 131
Db |||||||
61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGGKLEIK 107

RESULT 14

US-10-010-729-21
; Sequence 21, Application US/10010729
; Publication No. US2003018587A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-21

Query Match 77.5%; Score 534; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 NIWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84
Db |||||||
1 NIWMTQSPKSMNSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60
QY 85 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGG 125
Db |||||||
61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGG 101

RESULT 15

US-09-874-141-47

; Sequence 47, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized VL#2 amino acid
US-09-874-141-47

Query Match 77.2%; Score 532; DB 10; Length 133;
Best Local Similarity 75.8%; Pred. No. 1.4e-41;
Matches 100; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
QY 1 MGKIMESQTLVFISILLWLYGADGNIVMTQSPKSMNSVGERVTLTKKASENVTVVSWY 60
Db |||||||
1 MGFKMESQFLAFVAFALWLSGVDGIVMTQSPDLSLAVSLGERATINCKASQNVITAVMY 60
QY 61 QOKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGYSYPY 120
Db |||||||
61 QOKPEQSPKLLIYGASNRYTGVPDRFSGSGCTDFTLTISVQAEADVADYFCQYNSYPY 120
QY 121 TFGGCTKLEIKR 132
Db |||||||
121 TFGGCTKLEIKR 132

Search completed: May 25, 2005, 16:06:55
Job time : 52.0292 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 689

Sequence: 1 MGIMESQTLVFIILLWL.....GGYSYPYTFGGYKLEIKR 132

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	96.7	136	1 KW521	Ig kappa chain pre
2	615	89.3	118	2 I33932	Ig kappa chain pre
3	556	80.7	111	2 D37266	Ig kappa chain v r
4	515	74.7	107	2 S33132	Ig kappa chain v r
5	496	72.0	149	1 KW511	Ig kappa chain pre
6	495	71.8	152	2 S30751	Ig kappa chain pre
7	494	71.7	107	2 S38713	Ig light chain v r
8	474	68.8	128	2 A47159	Ig lambda chain v r
9	471	68.4	127	2 S04577	Ig kappa chain pre
10	470	68.2	131	2 PU0207	anti-idiotypic ant
11	467	67.8	135	2 S38807	Ig light chain v-j
12	465	67.5	117	2 S42466	Ig kappa chain v r
13	459	66.6	107	2 PU0268	Ig kappa chain v r
14	454	65.9	96	2 PH1070	Ig light chain v r
15	447	64.9	240	2 S06084	Ig kappa chain pre
16	446.5	64.8	91	2 PH1071	Ig light chain v r
17	445	64.6	108	2 PU0204	anti-DNA autoantib
18	442	64.2	134	2 PC1214	Ig kappa chain pre
19	441	64.0	134	1 K4HUI7	Ig kappa chain pre
20	436	63.3	119	2 P00265	Ig kappa chain v r
21	435	63.1	134	2 S49531	anti-Sm antibody v
22	432	62.7	107	2 S32192	Ig kappa chain v r
23	430	62.4	145	2 PU0014	Ig kappa chain pre
24	429.5	62.3	133	2 P50023	Ig kappa chain pre
25	428.5	62.2	103	1 K4HUI1	Ig kappa chain pre
26	427	62.0	107	2 S32191	Ig kappa chain v r
27	426.5	61.9	225	2 S37484	Ig kappa chain - m
28	422	61.2	132	2 S46373	Ig kappa chain v-j
29	419	60.8	129	2 S52793	Ig kappa chain v r

ALIGNMENTS

RESULT 1

KW521

Ig kappa chain precursor V region (MOPC 21) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A93736; A90262; B49982; A01917

R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.

Nucleic Acids Res. 9, 4485-4494, 1981

A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxy

A:Reference number: A93736; MUID:82059477; PMID:6170937

A:Accession: A93736

A:Molecule type: mRNA

A:Residues: 1-136 <HAM>

A:Cross-references: UNIPROT:P01634

R:Swastli, J.; Milstein, C.

Biochem. J. 128, 427-444, 1972

A:Title: The complete amino acid sequence of a mouse kappa light chain.

A:Reference number: A90262; MUID:73053310; PMID:4638343

A:Contents: myeloma protein MOPC 21

A:Accession: A90262

A:Molecule type: protein

A:Residues: 30-136 <SVA>

R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.

J. Biol. Chem. 269, 2805-2813, 1994

A:Title: Topology of an amiloride-binding protein.

A:Reference number: A49982; MUID:94132051; PMID:8300613

A:Accession: B49982

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 30-136 <LIN>

A:Cross-references: GB:L24803; NID:G452098; PIDN:AAC37684.1; PID:G452099

A:Experimental source: clone BA7.1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>

F:45-119/Domain: immunoglobulin homology <IMM>

F:125-136/Region: J segment (JK2)

F:52-117/Disulfide bonds: #status predicted

Query Match 96.7%; Score 666; DB 1; Length 136;

Best Local Similarity 96.5%; Pred. No. 4.2e-49;

Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGIMESQTLVFIILLWL.....GGYSYPYTFGGYKLEIKR 60

Db 6 MGIMESQTLVFIILLWL.....GGYSYPYTFGGYKLEIKR 65

Qy 61 QKPEQSKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGGYGYPY 120

Db 66 QOKPEQPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYPY 125

QY 121 TFGGGTKLEIK 131

Db 126 TFGGGTKLEIK 136

RESULT 2

I33932 Ig kappa chain precursor V region (E7) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C:Accession: I33932

R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l

A:Reference number: A33932; MUID:89282823; PMID:2499887

A:Accession: I33932

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-118 <BAC>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 615; DB 2; Length 118;

Best Local Similarity 100.0%; Pred. No. 6.9e-45;

Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIKMESQTLVFISILLWLXGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQ 61

Db 1 GIKMESQTLVFISILLWLXGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQ 60

QY 62 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYP 119

Db 61 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYP 118

RESULT 3

D37266

Ig kappa chain V region (129) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000

C:Accession: D37266

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A:Title: Heavy and light chain variable region sequences and antibody properties of anti

A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: D37266

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-111 <RUF>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 556; DB 2; Length 111;

Best Local Similarity 98.1%; Pred. No. 5.8e-40;

Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 84

Db 4 DIVMTQIPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 63

QY 85 RFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYPYTFGGGKLEIKR 132

Db 64 RFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYPYTFGGGKLEIKR 111

RESULT 4

S33132

Ig kappa chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S33132

R:Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Mar

submitted to the EMBL Data Library, May 1993

A:Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act

A:Reference number: S33131

A:Accession: S33132

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <TEM>

A:Cross-references: EMBL:222670; NID:G297473; PIDN:CAA80379.1; PID:G297474

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 515; DB 2; Length 107;

Best Local Similarity 92.5%; Pred. No. 1.6e-36;

Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 84

Db 1 NIVMTQSPKSMMSGVGVTLTKKASENVDTFVSWYQKPEQSPKLLIYGASNRVTGVPD 60

QY 85 RFTGSGSATDFTLTSSVQAEDLADYHCGQGYSYPYTFGGGKLEIK 131

Db 61 RFTGSGSATDFTLTSSVQAEDLADYHCGQSYPYFPTLGGGKLEIK 107

RESULT 5

KVMS11

Ig kappa chain precursor V region (MPC11) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

A:Accession: A90823; A90753; A90298; A01916

R:Kelley, D.E.; Coleclough, C.; Perry, R.P.

Cell 29, 681-689, 1982

A:Title: Functional significance and evolutionary development of the 5'-terminal region

A:Reference number: A90823; MUID:83001944; PMID:6288267

A:Accession: A90823

A:Molecule type: DNA

A:Residues: 1-71 <REL>

A:Cross-references: UNIPROT:P01633

A>Note: the sequence was determined from the differentiated gene

R:Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.

Can. J. Biochem. 58, 176-187, 1980

A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.

A:Reference number: A90753; MUID:80176554; PMID:6245773

A:Accession: A90753

A:Molecule type: mRNA

A:Residues: 41-149 <RAB>

R:Smith, G.P. 171, 337-347, 1978

Biochem. J. 171, 337-347, 1978

A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC 11.

A:Reference number: A90298; MUID:78186617; PMID:418775

A:Contents: myeloma protein MPC11

A:Accession: A90298

A:Molecule type: protein

A:Residues: 30-149 <SMI>

A>Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not d

C:Comment: The mature chain has 12 additional residues at its amino end, due to a tandem

42 corresponds to the amino-terminal residue of typical kappa chains.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: duplication; heterotetramer; immunoglobulin

F:1-23/Domain: signal sequence #status predicted <SIG>

F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>

F:57-131/Domain: immunoglobulin homology <IMM>

F:64-129/Disulfide bonds: #status predicted

Query Match 72.0%; Score 496; DB 1; Length 149;

Best Local Similarity 70.1%; Pred. No. 8.5e-35;

Matches 101; Conservative 10; Mismatches 21; Indels 12; Gaps 1;

QY	1	MGIKMESQTLVFTSILILWL-----YGADGNIVMTQSPKSMNSVGERVTLTCK	48
Db	6	MGIKMESQIQVFEVFLWLSGVDGDIIVMTQFAGVDGDIVMTQSHKFMSTSVGDRVSITCK	65
QY	49	ASENNVTVVSWYQOKPQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQASDLA	108
Db	66	ASQDVSTTAWYQOKPQSPKLLIYSARYTGVDRFTGSGGTDFTLTISVQASDLA	125
QY	109	DYHCGQGSYPYTFGGGTKLEIKR	132
Db	126	VYVYCOQHYSTPTTFGGGTKLEIKR	149
RESULT 6			
S30751	Ig kappa chain precursor V region - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000		
C;Accession:	S30751		
R;Grant,	F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.		
Nucleic Acids Res.	15, 5496, 1987		
A;Title:	Improved RNA sequencing method to determine immunoglobulin mRNA sequence.		
A;Reference number:	S30751; MUID:87260030; PMID:3601683		
A;Accession:	S30751		
A;Molecule type:	mRNA		
A;Residues:	1-152 <GRA>		
A;Cross-references:	EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID:g52196		
C;Superfamily:	immunoglobulin V region; immunoglobulin homology		
C;Keywords:	heterotetramer; immunoglobulin		
F;45-119/Domain:	immunoglobulin homology <IMW>		
F;138-152/Domain:	C region (C-kappa) (fragment) #status predicted <CRE>		
Query Match	71.8%; Score 495; DB 2; Length 152;		
Best Local Similarity	72.7%; Pred. No. 1e-34;		
Matches	96; Conservative 14; Mismatches 22; Indels 0; Gaps 0;		
QY	1	MGIKMESQTLVFTSILILWLYGADGNIVMTQSPKSMNSVGERVTLTCKASENVTVYSWY	60
Db	6	MGIKMESQIQAFVFLWLSGVDGDIIVMTQSHRPMSTSVGDRVSITCKASQDVTAVSWY	65
QY	61	QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEIDLADYHCGQGSYPY	120
Db	66	QOKPEQSPKLLIFWASTRTGVPDRFTGSGGTDYTLTISVQAEIDLALYYCQHYSTPL	125
QY	121	TFGGGTKLEIKR	132
Db	126	TFGAGTKLEIKR	137
RESULT 7			
S38713	Ig light chain V region - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000		
C;Accession:	S38713		
R;Cimanis,	A.Y.		
submitted to the	EMBL Data Library, November 1993		
A;Reference number:	S38713		
A;Accession:	S38713		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-107 <CIM>		
A;cross-references:	EMBL:X76019; NID:g416090; PIDN:CAA53606.1; PID:g1333952		
C;Superfamily:	immunoglobulin V region; immunoglobulin homology		
C;Keywords:	immunoglobulin		
F;16-90/Domain:	immunoglobulin homology <IMW>		
Query Match	71.7%; Score 494; DB 2; Length 107;		
Best Local Similarity	88.8%; Pred. No. 9e-35;		
Matches	95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;		
QY	25	NIIVMTQSPKSMNSVGERVTLTCKASENVTVYSWYQOKPEQSPKLLIYGASNRVTGVPD	84

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGG 124
 Db 61 GQSPKLLIYGASNRVTGVPDRFTGSGSGTDFLTISVQVEDLAVYFCQHHSSPWTFGG 120
 QY 125 GTKLEIK 131
 Db 121 GTKLEIK 127

RESULT 10
 PL0207
 anti-idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: PL0207
 R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
 Mol. Immunol. 27, 429-433, 1990
 A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reacting
 A:Reference number: PL0207; MUID:90309764; PMID:1973259
 A:Accession: PL0207
 A:Molecule type: mRNA
 A:Residues: 1-131 <SOU>
 A>Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:36-110/Domain: immunoglobulin homology <IMM>
 F:44-54/Region: complementarity-determining 1
 F:70-76/Region: complementarity-determining 2
 F:109-117/Region: complementarity-determining 3
 F:116-127/Region: J region

Query Match 68.2%; Score 470; DB 2; Length 131;
 Best Local Similarity 71.1%; Pred. No. 1.1e-32; Mismatches 20; Indels 0; Gaps 0;
 Matches 91; Conservative 17

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVWYQKRP 64
 Db 1 METKQVFYMLLLSLGSEGDIVMTQSHKFMSTVGDVSIICKASQDVRIAVWYQKRP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGG 124
 Db 61 GQSPKLLIYWASTRHGTGVPDRFTGSGSGTDFLTISNVQSEDLADYFCQHCQSYSPPTFGS 120

QY 125 GTKLEIKR 132
 Db 121 GTKLEIKR 128

RESULT 11
 S39807
 Ig light chain V-J region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S39807
 R:Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.
 Immunogenetics 36, 15-21, 1992
 A:Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2
 A:Reference number: S39807; MUID:92267566; PMID:1587549
 A:Accession: S39807
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <SEQ>
 A:Cross-references: EMBL:X59816
 A>Note: the authors translated the codon GGC for residue 1 as Ala and TGT for residue 21
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:38-118/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 467; DB 2; Length 135;
 Best Local Similarity 66.9%; Pred. No. 2.1e-32;
 Matches 89; Conservative 19; Mismatches 19; Indels 6; Gaps 1;

QY 4 KMESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVV-----TVV 57

Db 2 KMESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVWYQKRP 61
 QY 58 SWYQKQPOSPPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQYS 117
 Db 62 AWYQKQPGQPPKLLIYGASTRESGVDRFTGSGSGTDFLTISVQAEADLAVYVCQNDHS 121
 QY 118 YPYTFGGGTGLEI 130
 Db 122 YPYTFGGGTGLEI 134

RESULT 12
 S42466
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S42466
 R:Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: S42466
 A:Accession: S42466
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHI>
 A:Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 67.5%; Score 465; DB 2; Length 117;
 Best Local Similarity 76.9%; Pred. No. 2.7e-32;
 Matches 90; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 15 ILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVWYQKQSPKLLIYG 74
 Db 1 MLLWLSGVEGDIVMTQSHKFMSTVGDVSIICKASQDVGTAVWYQKQSPKLLIYW 60

QY 75 ASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGGGTGLEIK 131
 Db 61 ASSTRHTGVPDRFTGSGSGTDFLTISNVQSEDLADYFCQYSSYPYTFGGGTGLEIK 117

RESULT 13
 PL0268
 Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PL0268
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.
 J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0268
 A:Molecule type: mRNA
 A:Residues: 1-107 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:24-34/Region: complementarity-determining 1
 F:35-49/Region: framework 2
 F:50-56/Region: complementarity-determining 2
 F:57-88/Region: framework 3
 F:89-97/Region: complementarity-determining 3
 F:98-107/Region: framework 4

Query Match 66.6%; Score 459; DB 2; Length 107;
 Best Local Similarity 82.2%; Pred. No. 7.8e-32;
 Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSVGERVTLTKKASENVVTVSVWYQKQSPKLLIYGASNRVTGVPD 84

Db 1 NIVWAFKSMMSVGERVTLSCASENVGTYSWYQQTPEQSPQLLIYRASDRYFGVDP 60
Qy 85 RFTGSGSATDFTLTSSVQAEADLADYHCGQGSYSPYTFGGGKLEIK 131
Db 61 RFAGSGSAADFSLTSSVHAEDLADYCEQSYNPYTFGGGKLEVK 107

RESULT 14
PH1070
Ig light chain V region (clone 17s.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1070
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1070
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-96 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 454; DB 2; Length 96;
Best Local Similarity 93.9%; Pred. No. 1.8e-31;
Matches 92; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
Qy 25 NIVMTQSPKSMMSVGERVTLTCASENVTVYSWYQKPEQSPKLLIYGASNRYTGVPD 84
Db 1 NIVMTQSPKSMMSVGERVTLSCASENVGTYSWYQKPEQSPKLLIYGASNRYTGVPD 60

Qy 85 RFTGSGSATDFTLTSSVQAEADLADYHCGQGSYSPYTF 122
Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQ-YS-PRTF 96

RESULT 15
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 447; DB 2; Length 240;
Best Local Similarity 65.7%; Pred. No. 1.8e-30;
Matches 88; Conservative 15; Mismatches 25; Indels 6; Gaps 1;
Qy 5 MESQTLVPISTLLWLGADNIVMTQSPKSMMSVGERVTLTCASE-----NVVTYVS 58
Db 1 MESQTLVMSLLWISGTCGDFVMTQSPSSLAVSAGETVTLNCKSSQSLFYSGNQKNYLA 60

Qy 59 WYQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSY 118
Db 61 WYQKPEQSPKLLIYWASTROSGVDPDRFIGSGSGTDFTLTSSVQAEADLAIYCLQYET 120

Qy 119 PYTFGGGKLEIKR 132

Db 121 PYTFGAGTKLELKR 134

Search completed: May 25, 2005, 16:48:41
Job time : 18.6642 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.3423 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 699

Sequence: 1 MGIMESQTLVFISILLWL.....GGYSYPYTRGGGFKLEIKR 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	96.7	136	1 KV5B_MOUSE	P01634 mus musculus
2	496	72.0	149	1 KV5A_MOUSE	P01633 mus musculus
3	442	64.2	134	1 KV4C_HUMAN	P06314 homo sapien
4	428.5	62.2	133	1 KV4B_HUMAN	P06313 homo sapien
5	411	59.7	108	2 QAVIJO	Q8vi10 mus musculus
6	408	59.2	114	1 KV1A_MOUSE	P01632 mus musculus
7	403	58.5	236	2 QGGMW1	Q6gmw1 homo sapien
8	401	58.2	131	1 KV3I_MOUSE	P01661 mus musculus
9	401	58.2	255	2 Q6KB05	Q6kb05 mus musculus
10	400	58.1	236	2 Q6GMX8	Q6gmx8 homo sapien
11	399	57.9	236	2 Q6GMX0	Q6gmx0 homo sapien
12	394.5	57.3	129	1 KV3M_HUMAN	P18136 homo sapien
13	393.5	57.1	129	1 KV3L_HUMAN	P18135 homo sapien
14	392	56.9	121	1 KV4O_HUMAN	P06312 homo sapien
15	390	56.6	236	2 Q6GMX9	Q6gmx9 homo sapien
16	389	56.5	236	2 Q6PIH7	Q6pih7 homo sapien
17	388	56.3	114	1 KV4A_HUMAN	P01625 homo sapien
18	388	56.3	129	1 KV1W_HUMAN	P04431 homo sapien
19	388	56.3	234	2 Q7Z473	Q7z473 homo sapien
20	385	55.9	132	1 KV3F_MOUSE	P01658 mus musculus
21	384	55.7	238	2 Q66JS7	Q66js7 mus musculus
22	382.5	55.5	129	1 KV3H_HUMAN	P04207 homo sapien
23	382.5	55.5	235	2 Q6GMW0	Q6gmw0 homo sapien
24	381	55.3	236	2 Q6PIL8	Q6pil8 homo sapien
25	380.5	55.2	235	2 Q6GMV9	Q6gmv9 homo sapien
26	380	55.2	108	1 KV1M_HUMAN	P01605 homo sapien
27	378.5	54.9	235	2 Q6PJF2	Q6pjf2 homo sapien
28	378	54.9	99	2 Q5JL74	Q5jl74 mus musculus
29	378	54.9	236	2 Q6PIT5	Q6pit5 homo sapien
30	377	54.7	129	1 KV1X_HUMAN	P04432 homo sapien
31	377	54.7	236	2 Q6P5S8	Q6p5s8 homo sapien

RESULT 1
KV5B_MOUSE
ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Ig kappa chain V-V region MOPC 21 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the dideoxynucleotide method of RNA sequencing."
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIN; A93736; KVM521.
DR PDB; 1IGC; X-ray; L=..
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 Ig kappa chain V-V region MOPC 21.
FT DOMAIN 30 52 Framework-1.
FT DOMAIN 53 63 Complementarity-determining-1.
FT DOMAIN 64 78 Framework-2.
FT DOMAIN 79 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DOMAIN 118 126 Complementarity-determining-3.
FT DOMAIN 127 136 Framework-4.
FT STRAND 34 36

ALIGNMENTS

32 375.5 54.5 107 2 Q96SA9
33 375 54.4 108 1 KV1Y_HUMAN
34 375 54.4 237 2 Q7S236
35 374 54.3 108 2 Q9UL77
36 372 54.0 236 2 Q7Z3Y4
37 371.5 53.9 109 2 Q9UL78
38 371 53.8 244 2 Q85ZC8
39 369 53.6 108 1 KV1O_HUMAN
40 369 53.6 128 1 KV3K_HUMAN
41 368.5 53.5 109 2 Q9UL85
42 368 53.4 108 1 KV1V_HUMAN
43 368 53.4 240 2 Q65ZC9
44 366 53.1 236 2 Q7TS98
45 364 52.8 108 1 KV1H_HUMAN

Q96SA9 homo sapien
P80162 homo sapien
P78236 xenopus lae
Q9UL77 homo sapien
Q7Z3Y4 homo sapien
Q9UL78 homo sapien
Q85ZC8 homo sapien
P01607 homo sapien
P06311 homo sapien
Q9UL85 homo sapien
P04430 homo sapien
Q65ZC9 homo sapien
Q7LS98 mus musculu
P01600 homo sapien

FT STRAND 41 43
 FT TURN 44 45
 FT STRAND 48 53
 FT TURN 59 60
 FT STRAND 62 67
 FT TURN 69 70
 FT STRAND 74 78
 FT TURN 79 81
 FT STRAND 82 83
 FT TURN 85 86
 FT TURN 89 90
 FT STRAND 93 95
 FT STRAND 99 104
 FT TURN 110 111
 FT STRAND 113 119
 FT STRAND 126 127
 FT STRAND 132 136
 FT NON_TER 136 136
 SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;
 Query Match 96.7%; Score 666; DB 1; Length 136;
 Best Local Similarity 98.5%; Pred. No. 6.4e-60;
 Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MGIKMESQTLVPIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSWY 60
 DB 6 MGIKMESHTLVPIISILLCLYLGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSWY 65
 QY 61 QKQPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
 DB 66 QKQPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125
 QY 121 TFGGGTKLEIK 131
 DB 126 TFGGGTKLEIK 136

RESULT 2
 KV5A_MOUSE STANDARD; PRT; 149 AA.
 ID KV5A_MOUSE
 AC P01633;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region MPC11 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE OF 1-71 FROM N.A.
 RX MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;
 RA Kelley D.E., Coleclough C., Perry R.P.;
 RT "Functional significance and evolutionary development of the 5'-
 RT terminal regions of immunoglobulin variable-region genes.";
 RL Cell 29:681-689(1982).
 RN [2]
 RP SEQUENCE OF 41-149 FROM N.A.
 RX MEDLINE=80176554; PubMed=6245773;
 RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
 RT "The variability, arrangement, and rearrangement of immunoglobulin
 RT genes.";
 RL Can. J. Biochem. 58:176-187(1980).
 RN [3]
 RP SEQUENCE OF 30-149.
 RX MEDLINE=78186617; PubMed=418775;
 RA Smith G.P.;
 RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
 RT myeloma MPC 11.";
 RL Biochem. J. 171:337-347(1978).
 CC -!- MISCELLANEOUS: The mature chain has 12 additional residues at its
 CC amino end, due to a tandem duplication of 36 nucleotides after the
 CC codon for residue 36. Residue 42 corresponds to the amino-terminal

CC residue of typical kappa chains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J00561; AAA38776.1; -.
 DR PIR; A90823; KVMG11.
 DR HSP; P01634; IIGC.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region; Repeat; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 149
 FT DOMAIN 42 64
 FT DOMAIN 65 75
 FT DOMAIN 76 90
 FT DOMAIN 91 97
 FT DOMAIN 98 129
 FT DOMAIN 130 138
 FT DOMAIN 139 148
 FT REPEAT 26 35
 FT REPEAT 38 47
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;
 Query Match 72.0%; Score 496; DB 1; Length 149;
 Best Local Similarity 70.1%; Pred. No. 1.6e-42;
 Matches 101; Conservative 10; Mismatches 21; Indels 12; Gaps 1;
 QY 1 MGIKMESQTLVPIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKCK 48
 DB 6 MGIKMESQIQVFFVFWLWLSGVGDIVMTQFAGVDGDIWMTQSHKPFMTSVGDRVSITCK 65
 QY 49 ASENVTYVSVYQKPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLA 108
 DB 66 ASQDVSTTVANVYQKPEQSPKLLIYASVRYTVGVDPDRFTGSGSGTDTFTTISVQAEADLA 125
 QY 109 DYHCGQGSYPYTFGGTKLEIKR 132
 DB 126 VYVYCOQHYSTPTFTFGGKLEIKR 149
 RESULT 3
 KV4C_HUMAN STANDARD; PRT; 134 AA.
 ID KV4C_HUMAN
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 RA Marsh P., Mills F., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
 RT probe.";
 RL Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

```

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
DR EMBL; X02990; CAA26733.1; -.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Framework-3.
FT DOMAIN 83 114 Complementarity-determining-2.
FT DOMAIN 115 121 Framework-3.
FT DOMAIN 122 133 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON_TER 134 By similarity.
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0739832 CRC64;

Query Match 64.2%; Score 442; DB 1; Length 134;
Best Local Similarity 63.4%; Pred. No. 4.e-37;
Matches 85; Conservative 23; Mismatches 20; Indels 6; Gaps 1;

Qy 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKASENVV-----TVVS 58
Db 1 MVLQTVFISILLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQILYSSDNKNYLA 60

Qy 59 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
Db 61 WYQKPGQPPKLLIYWASTRESGVDPDRFSGSGGTDFLTLSLQAEADVAVVYCOQYNNL 120

Qy 119 PYTFGGGTKLEIKR 132
Db 121 PWTFGQGTKEIKR 134

RESULT 4
KV4B HUMAN STANDARD; PRT; 133 AA.
AC P0313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region JI.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 62.2%; Score 428.5; DB 1; Length 133;
Best Local Similarity 64.2%; Pred. No. 1e-35;
Matches 86; Conservative 21; Mismatches 20; Indels 7; Gaps 2;

Qy 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKASENVV-----TVVS 58
Db 1 MVLQTVFISILLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQILYSSNNKNYLA 60

Qy 59 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
Db 61 WYQKPGQPPKLLIYWASTRESGVDPDRFSGSGGTDFLTLSLQAEADVAVVYCOQYDTI 120

Qy 119 PYTFGGGTKLEIKR 132
Db 121 P-TFGGQGTKEIKR 133

RESULT 5
Q8VIJ0
ID Q8VIJ0 PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Name=Vk19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR PIR; A33933; A33933.
DR PIR; A37262; A37262.
DR PIR; PH1072; PH1072.

```



```
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC9E14B6559EFC9 CRC64;

Query Match 58.1%; Score 400; DB 2; Length 236;
Best Local Similarity 56.8%; Pred. No. 1.7e-32;
Matches 75; Conservative 29; Mismatches 26; Indels 2; Gaps 1;

QY 1 MGIKMSQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSWY 60
Db 1 MDMRVPQALLGL--LLMLPFGSCDIQMTQSPSSVSASVGDRTVITCRASQIGSSWLAWY 58

QY 61 QKQPEQSKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
Db 59 QKQPKGKAPNLLIYAASSLQSGVPSRFSGSGTDTLTISLQPEDFATYYCQQAHSFPF 118

QY 121 TFGGGTKLEIKR 132
Db 119 TFGGTVKDIKR 130

RESULT 11
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
```

```
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;

Query Match 57.9%; Score 399; DB 2; Length 236;
Best Local Similarity 57.6%; Pred. No. 2.1e-32;
Matches 76; Conservative 25; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGIKMSQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSWY 60
Db 1 MDMRVPQALLGL--LLMLRGCARDIQMTQSPSSVSASVGDRTVITCRASQINNYLWY 58

QY 61 QKQPEQSKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120
Db 59 QLKPGKAPNLLIYAASSLQSGVPSRFSGSGTDTLTISLURPDDFATYYCQGSYNIP 118

QY 121 TFGGGTKLEIKR 132
Db 119 TFGGTVNVEIKR 130

RESULT 12
QV3M_HUMAN STANDARD; PRT; 129 AA.
ID QV3M_HUMAN
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
```

```

RT mutation. Implications for etiology and immunotherapy. ";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR: P0021; K3HUHI.
DR HSSP; P01625; IREQ.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 57.3%; Score 394.5; DB 1; Length 129;
Best Local Similarity 58.9%; Pred. No. 3e-32;
Matches 76; Conservative 24; Mismatches 28; Indels 1; Gaps 1;

Qy 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKKASENV-VTVYVSWYQOK 63
Db 1 METPAQLFLLLWLPDPTTGIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

Qy 64 PEQSPKLLIYGASNRYTGVDPRTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFG 123
Db 61 PGQAPRLIYGAASSRATGIPDRFSGSGGTDTLTISRLEPDPFVAVYCCQYGGSPWTFG 120

Qy 124 GGTKLEIKR 132
Db 121 QGTKVEIKR 129

RESULT 13
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-1999 (Rel. 39, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=68171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy. ";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR: P0022; K3HUHA.
DR HSSP; P01625; IREQ.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; F:antigen binding; NAS.

```

```

DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 57.1%; Score 393.5; DB 1; Length 129;
Best Local Similarity 58.9%; Pred. No. 3.7e-32;
Matches 76; Conservative 24; Mismatches 28; Indels 1; Gaps 1;

Qy 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKKASENV-VTVYVSWYQOK 63
Db 1 METPAQLFLLLWLPDPTTGIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQOK 60

Qy 64 PEQSPKLLIYGASNRYTGVDPRTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFG 123
Db 61 PGQAPRLIYGAASSRATGIPDRFSGSGGTDTLTISRLEPDPFVAVYCCQYGGSPWTFG 120

Qy 124 GGTKLEIKR 132
Db 121 QGTKVEIKR 129

RESULT 14
KV40_HUMAN
ID KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1; (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; K4HU.
DR HSSP; P01625; ILVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO:0005576; C:extracellular; NAS.

```

DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS0835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >121 Ig kappa chain V-IV region.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 60 Complementarity-determining-1.
 FT DOMAIN 61 75 Framework-2.
 FT DOMAIN 76 82 Complementarity-determining-2.
 FT DOMAIN 83 114 Framework-3.
 FT DOMAIN 115 121 Complementarity-determining-3.
 FT DISULFID 43 114 By similarity.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 56.9%; Score 392; DB 1; Length 121;
 Best Local Similarity 63.8%; Pred. No. 4.9e-32;
 Matches 77; Conservative 19; Mismatches 19; Indels 6; Gaps 1;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVV-----TYVS 58
 DB 1 MVLQTVFSLLLWISGAYGDIIVMTQSPSLAVSLGERATINCKSSQSVLYSSNNKNYLA 60
 QY 59 WYQKPEQPKLIYGASNRYTCVDPDRFTGSGSATDFTLTISVQAEADLADYHCGGYSY 118
 DB 61 WYQKPEQPKLIYWASTRESGVDPDRFSGSGGTDTLTISLQAEADVAVYCCQYYSY 120

QY 119 P 119

DB 121 P 121

RESULT 15

Q6GMX9 PRELIMINARY; PRT; 236 AA.
 AC Q6GMX9
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC073763; AAH73763.1; -.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 56.6%; Score 390; DB 2; Length 236;
 Best Local Similarity 62.7%; Pred. No. 1.7e-31;
 Matches 74; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 15 ILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSWYQKPEQSPKLIYG 74

DB 13 LLLCFPGARCDLQMTQSPSSLSASVGRVTITCRASQNVSRWLAWYQORPEKAPKSLIYA 72

QY 75 ASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGGKLEIKR 132

DB 73 TSSLHSGVPSRFPSSGSGGTDTLTITSSLPQEDFATVYCCQYNTYPLTFGGGKVEIKR 130

Search completed: May 25, 2005, 15:56:07
 Job time : 64.3423 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 65.8977 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773A-4

Perfect score: 739

Sequence: 1 MNFGSLFLVLKGVQCR.....DRGAWFFDVWGAGTTVTVSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	100.0	140	6	ABG74241 Mouse ant
2	605	81.9	462	6	AAO29869 Mouse ant
3	605	81.9	462	7	ADJ79787 TRA-8 ant
4	605	81.9	464	5	AAU72801 TRA-8 hea
5	599	81.1	138	2	AAR20064 MRK16-H C
6	592	80.1	247	2	AAW11917 Murine MA
7	587	79.4	140	5	AAU76122 Mouse mon
8	585.5	79.2	139	1	AAU76132 Mouse mAb
9	582	78.8	140	5	AAU76132 Mouse mAb
10	581	78.6	138	2	AAW03722 Anti-huma
11	581	78.6	138	3	AAU32404 Mouse ant
12	581	78.6	139	2	AAR30480 hCEA spec
13	581	78.6	144	5	ABB79730 Anti-Stre
14	580	78.5	140	5	AAU76133 Mouse mAb
15	577	78.1	139	2	AAR27053 Anti-CEA
16	573.5	77.6	137	2	AAW57592 Chimeric
17	573.5	77.6	137	2	AAW89625 Mouse hum
18	573.5	77.6	137	3	AAU77513 Mouse ant
19	573.5	77.6	137	4	AAU667102 Amino aci
20	573.5	77.6	137	4	AAU64775 Mouse ant
21	573.5	77.6	137	4	AAU63393 Amino aci
22	573.5	77.6	137	5	ABU95208 Mouse joi
23	573.5	77.6	137	6	ABJ36667 Angiogene
24	573.5	77.6	137	8	ADO33883 Murine pa
25	564.5	76.4	139	2	AAR52773 Murine KC

26	564.5	76.4	139	2	AARS2791	Aar52791 Murine KC
27	563	76.2	477	2	AAAR47450	Aar47450 T84.12 He
28	563	76.2	477	2	AAAR47453	Aar47453 chiT84.12
29	560	75.8	138	8	ADR47397	Adr47397 Heavy cha
30	559	75.6	138	8	ADR88408	Adr88408 Murine 3D
31	559	75.6	142	2	AAR30882	Aar30882 Antibody
32	558	75.5	138	4	AAAB81977	Aab81977 Gangliosid
33	558	75.5	138	5	ABG76924	Abg76924 Mouse 3D6
34	558	75.5	138	6	ABU11002	Abu11002 Modified
35	554	75.0	136	2	AAR56962	Aar56962 MAb A33 h
36	553.5	74.9	139	2	AAW21656	Aaw21656 Chimeric
37	553.5	74.9	139	6	ABG74247	Abg74247 Mouse ant
38	553	74.8	138	3	AAU32406	AAU32406 Mouse ant
39	553	74.8	158	8	ADL27491	Adl27491 Amino aci
40	552	74.7	138	2	AAR32246	Aar32246 BR55-2 mu
41	552	74.7	138	2	AAR32242	Aar32242 Chimeric
42	552	74.7	139	2	AAR31588	Aar31588 BR55-2 he
43	552	74.7	144	8	ADR47417	Adr47417 Heavy cha
44	551.5	74.6	141	8	ADO43555	Ado43555 Amino aci
45	551	74.6	136	2	AAAR06251	Aar06251 Variable

ALIGNMENTS

RESULT 1

ABG74241
ID ABG74241 standard; protein; 140 AA.

AC ABG74241;

DT 22-APR-2003 (first entry)

DE Mouse antibody MB3.6 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

XX US2002132983-A1.

XX 19-SEP-2002.

XX 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Junghans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16566.

XX New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 9; 35pp; English.

XX The invention relates to a chimeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody MB3.6 heavy chain variable region
 XX
 SQ Sequence 140 AA;

Query Match 100.0%; Score 739; DB 6; Length 140;
 Best Local Similarity 100.0%; Pred. No. 1.3e-61;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
 QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120
 DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120
 QY 121 DRGAWFFDVWGAGTTVTSS 140
 DB 121 DRGAWFFDVWGAGTTVTSS 140

RESULT 2

AAO29869
 ID AAO29869 standard; protein; 462 AA.

AC AAO29869;

XX 27-AUG-2003 (first entry)

DE Mouse anti-human DR5 antibody (TRA-8) heavy chain.

XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
 KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
 KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
 KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
 KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
 KW Crohn's disease; diabetes mellitus; antibody; mouse.

XX Mus sp.

XX WO2003037913-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035333.

XX 01-NOV-2001; 2001US-0346402P.

XX (UABR-) UAB RES FOUND.

PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;

XX WPI; 2003-441350/41.

XX N-PSDB; AAL60477.

XX New purified antibody that specifically binds a TNF-related apoptosis-
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
 PT rheumatoid arthritis.

XX Example 16; Page 224-225; 251pp; English.

XX The invention relates to an antibody that specifically binds a tumour
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 CC DR4 or DR5. Antibodies of the invention are useful for selectively
 CC inducing apoptosis in target cells expressing DR4, for inhibiting
 CC proliferation of target cells expressing DR4 or for treating cancer,

CC inflammatory disease or autoimmune disease in a subject e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
 CC glomerular nephritis. The present sequence is mouse anti-human DR5
 CC antibody (TRA-8) heavy chain
 XX
 SQ Sequence 462 AA;

Query Match 81.9%; Score 605; DB 6; Length 462;
 Best Local Similarity 85.0%; Pred. No. 2.1e-48;
 Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVVLKGVQCEVLMVSGGGLVKPGGSLKLSCAASGTFPSRYAMSWVRQTP 60
 QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120
 DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARRG- 119
 QY 121 DRGAWFFDVWGAGTTVTSS 140
 DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 3

ADJ79787

ID ADJ79787 standard; protein; 462 AA.

XX ADJ79787;

XX 06-MAY-2004 (first entry)

XX TRA-8 antibody heavy chain.

XX nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
 KW antiallergic; antiinflammatory; antidiabetic; haemostatic;
 KW neuroprotective; antifertility; immunosuppressive; dermatological;
 KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
 KW proliferation;
 KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
 KW TRAIL; synovial cell; lymphocyte; neutrophil;
 KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
 KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
 KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
 KW autoimmune hemolytic anemia; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
 KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
 KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anemia.

XX Homo sapiens.

XX WO2003038043-A2.

XX 08-MAY-2003.

XX 25-OCT-2002; 2002WO-US034420.

XX 01-NOV-2001; 2001US-0346402P.

XX 24-JUN-2002; 2002US-0391478P.

XX (UABR-) UAB RES FOUND.

XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;

XX Lobuglio AF, Buchsbaum DJ;

XX WPI; 2003-421518/39.

XX Inducing apoptosis and inhibiting proliferation of target cells
 PT expressing DR5, by contacting the target cell with an antibody that binds
 PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic

```

PT agents.
PS Example 16; SEQ ID NO 23; 274pp; English.
XX
XX
CC The invention relates to a method of selectively inducing apoptosis in
CC and inhibiting (M1) proliferation of target cells expressing DR5,
CC comprising contacting the cell with an antibody that specifically binds
CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC vitro apoptosis-inducing activity in the cell expressing DR5, and
CC contacting the cell with one or more therapeutic agents. M1 is useful for
CC inducing apoptosis in target cell and inhibiting proliferation of target
CC cell expressing DR5, where the target cell is an abnormally proliferating
CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC cell. M2 is useful for treating a subject having inflammatory and
CC autoimmune diseases. The inflammatory or autoimmune disease are selected
CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC protein used in the method of the invention.
XX
SQ Sequence 462 AA;

Query Match 81.9%; Score 605; DB 7; Length 462;
Best Local Similarity 85.0%; Pred. No. 2.1e-48;
Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLFLVLVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWVRTP 60
DB 1 MNFGSLFLVLVLKGVQCEVNLVSGGGLVKPGGSLKSCASGFTFSRYAMSWVRTP 60

QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSEDTAIYYCARGY 120
DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSEDTAIYYCARGY 119

QY 121 DRGAWFFDVWGAGTIVTVSS 140
DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 4
AAU72801
ID AAU72801 standard; protein; 464 AA.
AC AAU72801;
XX
XX 26-FEB-2002 (first entry)
XX
XX TRA-8 heavy chain.
XX
XX Tumor necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
XX TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;
XX autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
XX rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
XX Addison disease; scleroderma; Goodpasture's syndrome; sterility;
XX myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
XX allergy; arteriosclerosis; myocarditis; cardiomyopathy;
XX glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
XX Mus musculus.
XX
XX WO200183560-A1.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014151.
XX

```

```

PR 02-MAY-2000; 2000US-0201344P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
XX WPI; 2002-049338/06.
XX
XX N-PSDB; AAS97062.
XX
XX Novel antibody specific for tumor necrosis factor-related apoptosis-
XX inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
XX Claim 26; Page 198-199; 229pp; English.
XX
XX The invention describes a novel antibody which recognizes a tumour
XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
XX DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
XX activity to a cell expressing DR5 in vivo. It is also useful for
XX preparing a therapeutic for selective apoptosis of abnormal or
XX dysregulated cells, and for inhibiting cell proliferation in a cell,
XX preferably a human breast, ovary, colon, haematopoietic, prostate,
XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
XX also be administered e.g. paclitaxel, taxol or cycloheximide. The
XX antibody is used to treat an autoimmune disease, systemic lupus
XX erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
XX host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
XX Addison disease, scleroderma, Goodpasture's syndrome, multiple sclerosis,
XX haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
XX disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, rejection after organ transplantation,
XX and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
XX breast tissue. Peptides used to design primers for isolating heavy and
XX light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
XX shown in AAU72799 and AAU72800
XX
XX Sequence 464 AA;

Query Match 81.9%; Score 605; DB 5; Length 464;
Best Local Similarity 85.0%; Pred. No. 2.1e-48;
Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLFLVLVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWVRTP 60
DB 1 MNFGSLFLVLVLKGVQCEVNLVSGGGLVKPGGSLKSCASGFTFSRYAMSWVRTP 60

QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSEDTAIYYCARGY 120
DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSEDTAIYYCARGY 119

QY 121 DRGAWFFDVWGAGTIVTVSS 140
DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 5
AAR20064
ID AAR20064 standard; protein; 138 AA.
XX
XX AAR20064;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 27-MAR-1992 (first entry)
XX
XX MRK16-H chain.
XX
XX Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX
XX Homo; sapiens.
XX
XX Mus musculus.
XX
XX Chimeric.
XX

```

```

PN JP03254691-A.
XX
PD 13-NOV-1991.
XX
PF 02-MAR-1990; 90JP-00051563.
XX
PR 02-MAR-1990; 90JP-00051563.
XX
PA (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX
DR WPI: 1992-002461/01.
DR N-PSDB; AAQ20070.
XX
FT Chimera antibody against drug resistant cancer - comprises variable
FT region homologous to region in mouse monoclonal antibody and constant
FT region homologous to region in human immunoglobulin.
PS
PS Disclosure; Fig 4; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 138 AA;

Query Match 81.1%; Score 599; DB 2; Length 138;
Best Local Similarity 83.6%; Pred. No. 1.9e-48;
Matches 117; Conservative 7; Mismatches 14; Indels 2; Gaps 2;

QY 1 MNFGSLIFLVILKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSRYAMSWVRQTP 60
DB 1 MNFGSLIFLVILKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSRYAMSWVRQTP 60
QY 61 EKRLEWVATISSGGSHYYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCARPGY 120
DB 61 EKRLEWVATISSGGSHYYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCAR-YY 119

QY 121 DRGAWFFDVWGAGTTVTSS 140
DB 120 RYEAWFAS-WGQGLTLVTUSA 138

RESULT 6
AAW11917
ID AAW11917 standard; protein; 247 AA.
XX
AC AAW11917;
XX
XX 24-JUN-1997 (first entry)
XX
XX Murine MAb SK48-E26 heavy chain.
XX
KW Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;
KW chimeric antibody; antibody engineering; monoclonal antibody; MAB;
KW SK48-E26; inflammation; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT 20..49
FT /label= FR1
FT /note= "framework region 1"
FT

```

```

FT Region
FT 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1 (Claim 10,
FT page 48)"
FT 55..68
FT /label= FR2
FT /note= "framework region 2"
FT 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2 (Claim 10,
FT page 48)"
FT 86..117
FT /label= FR3
FT /note= "framework region 3"
FT 118..127
FT /label= CDR3
FT /note= "complementarity determining region 3 (Claim 10,
FT page 48)"
FT 128..138
FT /label= FR4
FT /note= "framework region 4"
FT 139..247
FT /label= Constant_region
FT
FT WO9501997-A1.
FT
FT 19-JAN-1995.
XX
XX 07-JUL-1994; 94WO-US007659.
XX
XX 09-JUL-1993; 93US-00090534.
XX
XX 04-MAR-1994; 94US-00206190.
XX
XX (SMIX ). SMITHKLINE BEECHAM CORP.
XX
XX Young PR, Gross MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
XX
XX WPI: 1995-066868/09.
XX N-PSDB; AAT51436.
XX
XX Recombinant and humanised chimeric antibodies against human interleukin-1
XX -beta - for preventing and treating interleukin-mediated inflammatory
XX disorders.
XX
XX Claim 5; Page 36-37; 62pp; English.
XX
XX Amino acid sequences of the heavy chain (AAW11917) and light chain
XX (AAW11918) of anti-human interleukin-1 beta (IL-1 beta) murine monoclonal
XX antibody (MAB) SK48-E26 were deduced from nucleic acids (AAT51436-37)
XX derived from hybridoma SK48-E26. The heavy and light chains, esp. the
XX complementarity determining region sequences, can be utilised in novel
XX recombinant chimeric and humanised antibodies (see also AAW11919-20)
XX useful for the treatment and prevention of IL-1 mediated inflammatory
XX disorders
XX
XX Sequence 247 AA;

Query Match 80.1%; Score 592; DB 2; Length 247;
Best Local Similarity 82.1%; Pred. No. 1.7e-47;
Matches 115; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVILKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSRYAMSWVRQTP 60
DB 1 MNFGSLIFLVILKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSRYAMSWVRQTP 60
QY 61 EKRLEWVATISSGGSHYYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCARPGY 120
DB 61 EKRLEWVATISSGGSHYYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMVHCARGGV 120
QY 121 DRGAWFFDVWGAGTTVTSS 140
DB 121 RRG--YFDVWGAGTTVTSS 138

```


RESULT 7
 AAU76122
 ID AAU76122 standard; protein; 140 AA.
 XX
 AC AAU76122;
 DT 08-MAY-2002 (first entry)
 XX
 DE Mouse monoclonal antibody 26-2F heavy chain variable region.
 XX
 KW Mouse; monoclonal antibody; heavy chain variable region; VH; angiogenin;
 KW 26-2F; angiogenesis; tumour; cancer; retinopathy; syphilis;
 KW ocular neovascular disease; vitamin A deficiency; macular degeneration;
 KW Kaposi's sarcoma; rheumatoid arthritis; mycobacterial infection;
 KW sickle cell anaemia; Paget's disease; autoimmune disease;
 KW osteoarthritis; graft versus host disease; autoimmune disease;
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Signal_peptide
 FT /label= Mature_VH
 FT Region 50..54
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 FT Region 59..85
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 FT Region 118..129
 FT /label= Complementarity_determining_region
 FT /note= "This region is specifically claimed in claim 3"
 XX
 PN US2002010320-A1.
 XX
 PD 24-JAN-2002.
 XX
 PP 05-APR-1999; 99US-00286240.
 XX
 PR 05-APR-1999; 99US-00286240.
 XX
 PA (FETT/) FETT J W.
 XX
 PI Fett JW;
 XX
 DR WPI; 2002-187790/24.
 DR N-PSDB; ABK15270.
 XX
 PT New antibody immunologically reactive to angiogenin useful for inhibiting
 PT angiogenesis and for treating conditions associated with abnormal
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
 PT arthritis.
 XX
 PS Claim 6; Page 14; 20pp; English.
 XX
 CC The invention relates to an antibody immunologically reactive to
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain
 CC nonhuman-derived complementarity determining regions having a binding
 CC affinity to the angiogenin or its fragment in combination with human
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
 CC included are an expression vector comprising a nucleic acid encoding the
 CC antibody and a host cell transformed with the vector. The antibody or its
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
 CC The antibody is useful for treating a tumour in humans, by inhibiting,
 CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
 CC ability of circulating tumour cell to form a vascularised tumour mass.
 CC The antibody is useful for treating a mammal with abnormal or unwanted
 CC angiogenesis, including cancer, and other diseases mediated by
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
 CC

retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
 and retrolental fibroplasia, and other diseases associated with corneal
 neovascularisation including epidemic keratoconjunctivitis, vitamin A
 deficiency, contact lens overwear, atopic keratitis, superior limbic
 keratitis, syphilis, mycobacteria infections, lipid degeneration,
 chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
 infections, herpes zoster infections, protozoan infections, Kaposi's
 sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
 Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
 graft rejection. Diseases associated with retinal/choroidal
 neovascularisation include macular degeneration, sickle cell anaemia,
 sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
 trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
 disease, transplant rejection, autoimmune diseases such as type I
 diabetes, multiple sclerosis, systemic lupus erythematosus, and
 myasthenia gravis. The present sequence is the heavy chain variable
 region of mouse monoclonal antibody 26-2F
 XX
 SQ Sequence 140 AA;
 Query Match 79.4%; Score 587; DB 5; Length 140;
 Best Local Similarity 80.7%; Pred. No. 2.6e-47;
 Matches 113; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MNFGSLFLVLKGVQCEVVVVEGGGFKVPGGSLKLSCAAAGFTTSRYAMSVWRQTP 60
 DB 1 MDFGLSWFLVLKGVQCEVLMVVEGGGLVKPGGSLKLSCAAAGFTTSRYAMSVWRQTP 60
 QY 61 EKRLFWATISSGSHYTPDSVKGRTISRDNAKNTLYLQWSSLRSEDATLYYCARPCY 120
 DB 61 EKRLFWATISSGSHYTPDSVKGRTISRDNAKNTLYLQWSSLRSEDATLYYCARPCY 120
 QY 121 DRGAFFPDVWGAGTTVTVSS 140
 DB 121 YGYATYMDWQGGTSVTVSS 140
 RESULT 8
 AAP90480
 ID AAP90480 standard; protein; 139 AA.
 XX
 AC AAP90480;
 XX
 DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 01-NOV-1989 (first entry)
 XX
 DE Chimeric monoclonal antibody to human carcinoembryonic antigen.
 XX
 KW Chimeric monoclonal antibody; light chain; heavy chain; variable region;
 KW human carcinoembryonic antigen; cell line CE25.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 50..56
 FT /label= CDR1H
 FT Region 71..84
 FT /label= CDR2H
 FT Region 117..126
 FT /label= CDR3H
 PN EP323806-A.
 XX
 PD 12-JUL-1989.
 XX
 PP 28-DEC-1988; 88EP-00810898.
 XX
 PR 05-JAN-1988; 88GB-000000077.
 PR 24-AUG-1988; 88GB-00020099.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX

PI Hardman N, Gill LL, Dewinter RFJ, Wagner K, Heusser C;
 XX WPI; 1989-200701/28.
 DR N-PSDB; AAN90301.
 XX
 PT Chimeric monoclonal antibody to human carcinoembryonic antigen -
 PT comprises variable regions of mouse origin and human constant regions,
 PT for cancer diagnosis and therapy.
 XX
 XX Claim 30; Page 37; 53pp; English.
 PS
 CC The peptide is expressed by the sequence of AAN90301. The heavy chain
 CC variable region is specific for human carcinoembryonic antigen. (Updated
 CC on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 139 AA;
 Query Match 79.2%; Score 585.5; DB 1; Length 139;
 Best Local Similarity 81.4%; Pred. No. 3.6e-47;
 Matches 114; Conservative 10; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MNFGSLIFLVILKGVQCEVVVSGGFGFKPGGSLKLSCAAAGFTFRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVILKGVQCEVLESGGGLVKPGGSLKLSCAASGFTFRYAMWVRQTP 60
 QY 61 EKRLWVATISSGGSHYYPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYICARPGY 120
 DB 61 EKRLWVATISSGGT-TYYPDSVKGRFTISRDNARNILYQVSSLSRSEDTAIYICARPGY 119
 QY 121 DRGAWFFDVGAGTTVTSS 140
 DB 120 DGYLYVDYWGQGTSLTVSS 139
 RESULT 9
 AAU76132
 ID AAU76132 standard; protein; 140 AA.
 XX
 AC AAU76132;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Mouse mAb 26-2F heavy chain variable region mutant M100Y.
 XX
 KW Mouse; angiogenesis; tumour; cancer; retinopathy;
 KW ocular neovascular disease; vitamin A deficiency; syphilis;
 KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;
 KW osteoarthritis; graft versus host disease; autoimmune disease;
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; mutant; mutein; monoclonal antibody; 26-2F;
 KW heavy chain variable region; M100Y.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19 /label= Signal_peptide
 FT Protein 20..140 /label= Mature_VH
 FT Misc-difference 100 /note= "Wild-type Met substituted by Tyr"
 FT
 XX
 XX US2002010320-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 05-APR-1999; 99US-00286240.
 XX
 PR 05-APR-1999; 99US-00286240.

XX
 PA (FETT/) FETT J W.
 XX Fett JW;
 PI
 XX WPI; 2002-187790/24.
 DR
 XX New antibody immunologically reactive to angiogenin useful for inhibiting
 PT angiogenesis and for treating conditions associated with abnormal
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
 PT arthritis.
 XX
 XX Claim 10; Page; 20pp; English.
 PS
 XX The invention relates to an antibody immunologically reactive to
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain
 CC nonhuman-derived complementarity determining regions having a binding
 CC affinity to the angiogenin or its fragment in combination with human
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
 CC included are an expression vector comprising a nucleic acid encoding the
 CC antibody and a host cell transformed with the vector. The antibody or its
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
 CC The antibody is useful for treating a tumour in humans, by inhibiting the
 CC ability of circulating tumour cell to form a vascularised tumour mass.
 CC The antibody is useful for treating a mammal with abnormal or unwanted
 CC angiogenesis, including cancer, and other diseases mediated by
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
 CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
 CC and retrolental fibroplasia, and other diseases associated with corneal
 CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
 CC deficiency, contact lens overwear, atopic keratitis, superior limbic
 CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
 CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
 CC infections, herpes zoster infections, protozoan infections, Kaposi's
 CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
 CC Wegener's sarcoidosis, scleritis, Steven Johnson's disease, and corneal
 CC graft rejection. Diseases associated with retinal/choroidal
 CC neovascularisation include macular degeneration, sickle cell anaemia,
 CC sarcoid, Paget's disease, mycobacterial infections, Behcet's disease,
 CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
 CC disease, transplant rejection, autoimmune diseases such as type I
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
 CC myasthenia gravis. The present sequence represents the M100Y mutant of
 CC the mouse monoclonal antibody 26-2F light chain variable region. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer using the sequence appearing as AAU76122 and the information
 CC in the claims
 XX
 SQ Sequence 140 AA;
 Query Match 78.8%; Score 582; DB 5; Length 140;
 Best Local Similarity 80.0%; Pred. No. 7.7e-47;
 Matches 112; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MNFGSLIFLVILKGVQCEVVVSGGFGFKPGGSLKLSCAAAGFTFRYAMSWVRQTP 60
 DB 1 MDFGLSWVFLVILKGVQCEVNLVBSGGGLVKPGGSLKLSCAASGFTFSYTWVRQTP 60
 QY 61 EKRLWVATISSGGSHYYPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYICARPGY 120
 DB 61 EKRLWVATISSGGNTYYPDSVKGRFTISRDIKNTLYLQMSLSRSEDTALYYCTELGD 120
 QY 121 DRGAWFFDVGAGTTVTSS 140
 DB 121 YGVAYTMDYWGQGTSLTVSS 140
 RESULT 10
 AAU03722
 ID AAU03722 standard; protein; 138 AA.
 XX
 AC AAU03722;

XX 02-APR-1997 (first entry)
 DT Anti-human gp39 Mab 39-1.106 heavy chain variable region.
 DE Heavy chain; variable region; murine; mouse; anti-human; disease;
 DE glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder; immune;
 KW autoimmune; allergic response; organ rejection; drug; graft versus host;
 KW cell imaging; tumour; targeted; delivery; targeted.
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Peptide 20..138
 FT /label= mat_peptide
 FT Region 50..54
 FT /note= "complementarity determining region 1"
 FT Region 69..84
 FT /note= "complementarity determining region 2"
 FT Region 117..126
 FT /note= "complementarity determining region 3"
 XX
 XX WO9623071-A2.
 XX
 XX 01-AUG-1996.
 XX
 XX 26-JAN-1996; 96WO-US001119.
 XX
 XX 26-JAN-1995; 95US-00379057.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Siedak A, Hollenbaugh D, Gilliland LK, Gordon ML, Bajorath J;
 PI Aruffo AA, Harris LJ;
 XX
 XX WPI; 1996-362694/36.
 DR N-PSDB; AAT35974.
 XX
 XX Monoclonal antibodies specific for different epitope(s) on human gp39 -
 PT used for inhibiting B cell activation and for the diagnosis of various
 PT disorders, e.g. cancer, psoriasis etc..
 XX
 XX Claim 91; Fig 6B; 167pp; English.
 XX
 XX The present sequence is the heavy chain variable region of the murine
 CC anti-human glycoprotein (gp) 39 monoclonal antibody (MAB) 39-1.106 (a
 CC member of the murine III(D) subgroup). The MAB was prepd. by immunising a
 CC 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days
 CC later harvesting and fusing spleen and lymph cells to mouse melanoma
 CC cells, to produce an anti-human gp39 MAB producing hybridoma. The MAB may
 CC be useful for diagnosing disease states, inhibiting B-cell activation and
 CC for treating immunological disorders, e.g. autoimmune disorders, allergic
 CC responses, organ rejection and graft versus host disease. It may also be
 CC used for imaging cells which express gp39 on their surface, e.g. tumour
 CC cells, and to target therapeutic agents to such cells. The MAB inhibits
 CC the CD40/gp39 interaction, therefore limiting both prim. and sec.
 CC responses to T-cell dependent antigens and Ab prodn. specific to these
 CC antigens. A typical compen. for intramuscular injection pref. contains 50
 CC mg of MAB in 1 ml of sterile buffered water
 XX
 XX Sequence 138 AA;
 SQ
 Query Match 78.6%; Score 581; DB 2; Length 138;
 Best Local Similarity 81.4%; Pred. No. 9.4e-47;
 Matches 114; Conservative 10; Mismatches 14; Indels 2; Gaps 2;
 QY 1 MNFGSLFLVLVLKGVCEVVVSGGFKPGSLKLSCAAAGFTFSRVAMSWRQTP 60
 DB 1 MNFGSLFLVLVLKGVCEVVVSGGFKPGSLKLSCTTSGFTFNAMSWRQTP 60

QY 61 EKRLWVATISSGSHYTPDSVKGRFTTISRDNAKNTLYLQWSSLSRSDTAIYYCARQY 120
 DB 61 EKRLWVASISSGDS-TYTPDSVGRFTISRDNARNILYLQWSSLSRSDTAIYYCAR-HY 118
 QY 121 DRGAWFPDVMGAGTTVTVSS 140
 DB 119 DYDSIAMDYWCQGSVTVSS 138
 RESULT 11
 AAY32404
 ID AAY32404 standard; protein; 138 AA.
 XX
 XX AC AAY32404;
 XX
 XX DT 13-MAR-2000 (first entry)
 XX
 XX DE Mouse anti-verotoxin II antibody VTml-1 heavy chain variable region.
 XX
 XX KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
 KW monoclonal antibody; heavy chain; mouse; humanised antibody;
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome; HUS;
 KW therapy.
 XX
 XX OS Mus musculus.
 XX
 XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..138
 FT /note= "mature protein"
 FT Region 50..54
 FT /note= "complementarity determining region 1"
 FT Region 69..85
 FT /note= "complementarity determining region 2"
 FT Region 118..127
 FT /note= "complementarity determining region 3"
 XX
 XX WO9959629-A1.
 XX
 XX 25-NOV-1999.
 XX
 XX 19-MAY-1999; 99WO-US011179.
 XX
 XX 20-MAY-1998; 98US-0086570P.
 XX
 XX (TEIJ) TEIJIN LTD.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasesques M;
 PI
 XX WPI; 2000-086580/07.
 DR N-PSDB; AAZ35241.
 XX
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 XX producing E. coli.
 XX
 XX Claim 5; Fig 1a; 59pp; English.
 XX
 XX This sequence represents the heavy chain variable region of murine
 CC monoclonal antibody VTml-1 (MuVTml-1), an antibody that specifically
 CC binds to the B subunit of verotoxin II (VT2). The invention relates to
 CC humanised antibodies against VT2 that are capable of neutralizing VT2
 CC and/or VT2 variants. The humanised antibody is a humanized form of MuVTml
 CC -1 comprising the complementarity determining regions of MuVTml-1 and the
 CC heavy and light chain variable region frameworks from the human GF4
 CC antibody heavy and light chain frameworks, provided that at least 1
 CC position selected from L49, H29, H30, H49 and H98 is occupied by the
 CC amino acid at the equivalent position of the MuVTml-1 antibody heavy or
 CC light chain variable region framework. Such humanized antibodies (see
 CC AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times that of
 CC MuVTml-1. They are used for treating a patient suffering from, or at risk
 CC of, the toxic effects from VT2 (claimed), especially for treating

CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic
 CC uraemic syndrome (HUS)
 SQ Sequence 138 AA;

Query Match 78.6%; Score 581; DB 3; Length 138;
 Best Local Similarity 81.6%; Pred. No. 9.4e-47;
 Matches 115; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

QY 1 MNFGSLIFLVLVKGVCEVVVSGGGFVKPGGSLKLSCAAAGFTFSRYAMSWRQTP 60
 DB 1 MNFVLSIFLALILKGVCEVQVSGGGFVKPGGSLKLSCAAAGFTFSRYAMSWRQTP 60
 QY 61 EKRLWVAITSSGSHYTPDSVKGRFTISRDNKNTLYLQSSLSRSEDATYYCARPG 120
 DB 61 EKRLWVAITSSGSHYTPDSVKGRFTISRDNKNTLYLQSSLSRSEDATYYCARPG 119

QY 121 DRGAW-FFDVWAGTIVTVSS 140
 DB 120 --DAWGNDYWGQTSVTSS 138

RESULT 12
 AAR30480
 ID AAR30480 standard; protein; 139 AA.
 AC AAR30480;
 XX
 DT 06-MAY-1993 (first entry)
 XX
 DE hCEA specific mouse heavy chain variable chain region.
 XX
 KW Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;
 KW cancer.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT Protein 20..139
 FT Protein /note= "mature peptide"
 XX
 PN JP04330295-A.
 XX
 PD 18-NOV-1992.
 XX
 PF 28-DEC-1990; 90JP-00408811.
 XX
 PR 28-DEC-1990; 90JP-00408811.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 DR WPI; 1993-003502/01.
 DR N-PSDB; AAQ33052.
 XX
 PT Mouse-human chimeric antibody for diagnosis and treatment of cancer -
 PT obtd. by combining variable region of mouse antibody specifically
 PT combining to human cancer embryonic antigen with constant region of human
 PT antibody.
 XX
 PS Disclosure; Page 6; 10pp; Japanese.
 XX
 CC The sequence is that of the heavy chain variable region of a mouse
 CC antibody specific to human cancer embryonal antigen (hCEA). The region is
 CC used, with the corresponding mouse light chain variable region and the
 CC constant region of a human antibody, to prepare a mouse-human chimeric
 CC antibody which can be used for the diagnosis and treatment of cancer
 XX
 SQ Sequence 139 AA;

Query Match 78.6%; Score 581; DB 2; Length 139;
 Best Local Similarity 83.7%; Pred. No. 9.5e-47;

Matches 118; Conservative 7; Mismatches 12; Indels 4; Gaps 3;

QY 1 MNFGSLIFLVLVKGVCEVVVSGGGFVKPGGSLKLSCAAAGFTFSRYAMSWRQTP 60
 DB 1 MNFVLSIFLALILKGVCEVQVSGGGFVKPGGSLKLSCAAAGFTFSRYAMSWRQTP 60
 QY 61 EKRLWVAITSSGSHYTPDSVKGRFTISRDNKNTLYLQSSLSRSEDATYYCARPG 119
 DB 61 EKRLWVAITSSGSHYTPDSVKGRFTISRDNKNTLYLQSSLSRSEDATYYCARVHY 119

QY 120 YDRGAWFFDVWAGTIVTVSS 140
 DB 120 YDSPA--MDYWGQTSVTSS 138

RESULT 13
 ABB79730
 ID ABB79730 standard; protein; 144 AA.
 XX
 AC ABB79730;
 XX
 DT 29-OCT-2002 (first entry)
 XX
 DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.
 XX
 KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
 KW antibody; anticaries; transgenic plant; transgenic animal; caries;
 KW immunotherapy; therapy.
 XX
 OS Mus musculus.
 XX
 PN US2002068066-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 15-JUN-2001; 2001US-00881823.
 XX
 PR 20-AUG-1999; 99US-00378577.
 XX
 PA (SHIW/) SHI W.
 PA (MORR/) MORRISON S L.
 PA (TRIN/) TRINH K.
 PA (WIMS/) WIMS L.
 PA (CHEN/) CHEN L.
 PA (ANDE/) ANDERSON M H.
 XX
 PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
 XX
 DR WPI; 2002-565838/60.
 DR N-PSDB; ABN84611.
 XX
 PT Treatment and prevention of dental caries in mammals, in particular
 PT humans by orally administering genetically engineered or purified
 PT antibodies that bind to surface antigens of carcinogenic organisms.
 XX
 PS Claim 14; Fig 3B; 30pp; English.
 XX
 CC The present sequence is the protein sequence of the heavy chain variable
 CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds
 CC specifically to the surface antigens of carcinogenic type c Streptococcus
 CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
 CC HB 12558) hybridoma cells. In an example from the invention, chimeric
 CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
 CC and human antibody constant regions. Such chimeric monoclonal antibodies
 CC can be used to prevent or treat dental caries in humans. The antibodies
 CC engage the effector apparatus of the human immune system when they bind
 CC carcinogenic organisms, resulting in their destruction. The chimeric
 CC antibodies may be produced in edible plants, in transgenic animals, or in
 CC chicken eggs for oral ingestion
 XX
 SQ Sequence 144 AA;

Query Match 78.6%; Score 581; DB 5; Length 144;

Best Local Similarity 76.8%; Pred. No. 9.9e-47;
Matches 109; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVVLKVGOCCEVVVVEGSGGFVKGSLKLSCAAGFTSRYAMSVWROTP 60
1 MFGSLIFLVVLKVGOCCEVVVVEGSGGFVKGSLKLSCAAGFTSRYAMSVWROTP 60
DB 61 EKRLVAVATISSGSHYTPDSVKGRFTISRDNANKTYLQWSLSRSEDTALYYCARPCY 120
61 EKRLVAVATISSGSHYTPDSVKGRFTISRDNANKTYLQWSLSRSEDTALYYCARPCY 120
QY 121 DRGAMFF--DVGAGTTVTVSS 140
121 DRGAMFF--DVGAGTTVTVSS 140
DB 121 SYGSYYAMDYWGQGTSTVTVSS 142
121 SYGSYYAMDYWGQGTSTVTVSS 142

RESULT 14
AAU76133
ID AAU76133 standard; protein; 140 AA.

AC AAU76133;
XX
XX 08-MAY-2002 (first entry)
DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX Mouse; angiogenesis; tumour; cancer; retinopathy;
XX ocular neovascular disease; vitamin A deficiency; syphilis;
XX Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;
XX sickle cell anaemia; Paget's disease; mycobacterial infection;
XX osteoarthritis; graft versus host disease; autoimmune disease;
XX type I diabetes; multiple sclerosis; systemic lupus erythematosus;
XX myaethenia gravis; mutant; monoclonal antibody; 26-2F;
XX heavy chain variable region; E59Y.

OS Mus sp.
OS Synthetic.

XX key Location/Qualifiers
FH Peptide 1..19
FT /label= signal_peptide
FT 20..140
FT Protein /label= Mature_VH
FT Misc-difference 59
FT /note= "Wild-type Glu substituted by Tyr"

PN US2002010320-A1.

XX 24-JAN-2002.

XX 05-APR-1999; 99US-00286240.

XX 05-APR-1999; 99US-00286240.

XX (FETT/) FETT J W.

XX Fect JW;

XX WPI; 2002-187790/24.

PT New antibody immunologically reactive to angiogenin useful for inhibiting
PT angiogenesis and for treating conditions associated with abnormal
PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
PT arthritis.

PS Claim 11; Page; 20pp; English.

CC The invention relates to an antibody immunologically reactive to
CC angiogenin or a fragment of angiogenin comprising light and heavy chain
CC nonhuman-derived complementarity determining regions having a binding
CC affinity to the angiogenin or its fragment in combination with human
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
CC included are an expression vector comprising a nucleic acid encoding the

CC antibody and a host cell transformed with the vector. The antibody or its
CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
CC The antibody is useful for treating a tumour in humans, by inhibiting,
CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
CC ability of circulating tumour cell to form a vascularised tumour mass.
CC The antibody is useful for treating a mammal with abnormal or unwanted
CC angiogenesis, including cancer, and other diseases mediated by
CC angiogenesis, including cancer neovascular disease, diabetic retinopathy,
CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
CC and retrolental fibroplasia, and other diseases associated with corneal
CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
CC deficiency, contact lens overwear, atopic keratitis, superior limbic
CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
CC infections, herpes zoster infections, protozoan infections, Kaposi's
CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
CC graft rejection. Diseases associated with retinal/choroidal
CC neovascularisation include macular degeneration, sickle cell anaemia,
CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
CC disease, transplant rejection, autoimmune diseases such as type I
CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
CC myaethenia gravis. The present sequence represents the E59Y mutant of the
CC mouse monoclonal antibody 26-2F light chain variable region. Note: The
CC present sequence is not shown in the specification but was created by the
CC indexers using the sequence appearing as AAU76122 and the information in
CC the claims

SQ Sequence 140 AA;

Query Match 78.5%; Score 580; DB 5; Length 140;
Best Local Similarity 80.0%; Pred. No. 1.2e-46;
Matches 112; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKVGOCCEVVVVEGSGGFVKGSLKLSCAAGFTSRYAMSVWROTP 60
1 MFGSLIFLVVLKVGOCCEVVVVEGSGGFVKGSLKLSCAAGFTSRYAMSVWROTP 60
DB 61 EKRLVAVATISSGSHYTPDSVKGRFTISRDNANKTYLQWSLSRSEDTALYYCARPCY 120
61 EKRLVAVATISSGSHYTPDSVKGRFTISRDNANKTYLQWSLSRSEDTALYYCARPCY 120
QY 121 DRGAMFFDVGAGTTVTVSS 140
121 DRGAMFFDVGAGTTVTVSS 140
DB 121 YGYAYTMDYWGQGTSTVTVSS 140
121 YGYAYTMDYWGQGTSTVTVSS 140

RESULT 15

XX AAR27053 standard; protein; 139 AA.

XX AAR27053;

XX 01-MAR-1993 (first entry)

XX Anti-CEA specific heavy chain variable region.

XX Human; carcinoembryonic antigen; heavy chain; light chain; variable;
XX region; diagnostic; tumour; markers; targeting.

OS Mus musculus.

XX key Location/Qualifiers

XX FH Peptide 1..19

XX FT /note= "signal peptide"

XX FT Protein 20..139

XX /note= "mature peptide"

XX JP04234987-A.

XX 24-AUG-1992.

PF 28-DEC-1990; 90JP-00408810.
 XX
 PR 28-DEC-1990; 90JP-00408810.
 XX
 PA (MITU) MITSUBISHI KASEI CORP.
 XX
 DR WPI; 1992-327631/40.
 DR N-PSDB; AAQ28746.
 XX
 PT New DNA fragments encoding variable regions of ABS specific for human CEA
 PT - for diagnosing and monitoring tumours, as tumour markers and for
 PT treatment of tumours.
 XX
 PS Disclosure; Fig 1; 7pp; Japanese.
 XX
 CC The anti-CEA murine monoclonal antibody heavy chain variable region was
 CC obt'd. by screening a cDNA library prep'd. from mRNA obt'd. from hybridomas
 CC producing anti-CEA-specific antibodies with a probe based on the constant
 CC region of the H-chain. The antibodies reacts specifically with human CEA
 CC and are useful as a diagnostic agents, as tumour markers for digestive
 CC organs, for diagnosis of malignant tumours, for monitoring after cancer
 CC operations, to follow up bloodless therapy or as therapeutic agents in
 CC passive immune therapy and targetting therapy. See also AAR27054
 XX
 SQ Sequence 139 AA;

Query Match 78.1%; Score 577; DB 2; Length 139;
 Best Local Similarity 83.0%; Pred. No. 2.3e-46;
 Matches 117; Conservative 8; Mismatches 12; Indels 4; Gaps 3;

QY 1 MNRGFSILFLVLVYKGVQCEVVVSGGCGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 |||||
 DB 1 MNRGFSILFLVLVYKGVQCEVVKLVESGGGLVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 |||||
 QY 61 EKRLWVATISSGSHYYPDSVKGRTISRDNKXNTLYLQMSLRSEDTAIYYCARPG- 119
 |||||
 DB 61 EKRLWVATISSGSHYYPDSVKGRTISRDNKXNTLYLQMSLRSEDTAIYYCARVHY 119
 |||||
 QY 120 YDRGAMFFDVWGAGTYTVSS 140
 |||||
 DB 120 YDSPA--MDYMGQGTSTVSS 138
 |||||

Search completed: May 25, 2005, 15:47:13
 Job time : 67.8977 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 17.4512 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-4

Perfect score: 739
Sequence: 1 MNFSPSLFLVLKGVCE.....DRGAFPDVWGAGTTVTSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	80.1	247	5	PCT-US94-07659-2
2	586.5	79.4	135	2	US-08-579-378A-16
3	581	78.6	138	2	US-08-579-057-14
4	566	76.6	135	3	US-08-579-183A-32
5	565.5	76.5	135	3	US-08-579-378A-20
6	565	76.5	136	3	US-08-976-183A-34
7	560	75.8	136	3	US-08-976-183A-31
8	559	75.6	136	3	US-08-976-183A-31
9	554	75.0	136	1	US-08-253-877C-57
10	554	75.0	136	1	US-08-452-164A-57
11	552	74.7	138	1	US-08-053-171-7
12	552	74.7	138	1	US-08-053-171-11
13	545.5	73.8	139	1	US-08-129-930B-96
14	545.5	73.8	139	3	US-08-134-346A-51
15	545.5	73.8	139	3	US-08-976-288A-96
16	538	72.8	140	3	US-08-836-561-23
17	538	72.8	140	3	US-09-434-122-23
18	538	72.8	158	2	US-08-653-402B-6
19	531	71.9	130	4	US-09-225-322B-8
20	531	71.9	130	4	US-09-225-322B-18
21	531	71.9	130	4	US-09-764-304-8
22	531	71.9	130	4	US-09-764-304-18
23	528.5	71.5	159	2	US-08-653-402B-2
24	527	71.3	119	4	US-08-875-674A-1
25	522	69.3	158	2	US-08-653-402B-10
26	512	69.3	119	4	US-08-875-674A-3
27	508	68.7	121	1	US-08-339-582-2

28	505.5	68.4	255	2	US-07-690-192-4	Sequence 4, Appl
29	504.5	68.3	123	1	US-08-356-272-3	Sequence 3, Appl
30	501	67.8	170	2	US-08-652-558-40	Sequence 40, Appl
31	496.5	67.2	135	5	PCT-US95-07302-8	Sequence 8, Appl
32	494	66.8	119	2	US-08-475-000-16	Sequence 16, Appl
33	494	66.8	119	2	US-08-483-199-16	Sequence 16, Appl
34	494	66.8	119	2	US-08-484-508-16	Sequence 16, Appl
35	491.5	66.5	135	3	US-08-619-491-8	Sequence 8, Appl
36	488	66.0	119	4	US-09-232-290-55	Sequence 55, Appl
37	487.5	66.0	463	4	US-09-472-087-4	Sequence 4, Appl
38	487.5	66.0	463	4	US-09-472-087-68	Sequence 68, Appl
39	486	65.8	123	3	US-09-344-587-13	Sequence 13, Appl
40	485.5	65.7	144	1	US-08-026-320A-2	Sequence 2, Appl
41	484.5	65.6	120	4	US-08-435-516-3	Sequence 3, Appl
42	484	65.5	142	1	US-08-305-683A-2	Sequence 2, Appl
43	483	65.4	239	2	US-08-553-497A-18	Sequence 18, Appl
44	483	65.4	464	4	US-09-472-087-2	Sequence 2, Appl
45	483	65.4	464	4	US-09-472-087-66	Sequence 66, Appl

ALIGNMENTS

```

RESULT 1
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Harle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; NUMBER OF INVENTIONS: 21
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sulton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-2
; Query Match      80.1%; Score 592; DB 5; Length 247;

```

Best Local Similarity 82.1%; Pred. No. 4.1e-54;
Matches 115; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVVVSGGFFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
Db 1 MNGLRILFVLVTLKGVKCEVHLVSGGGLVXPGGSLKLSCAAAGFTFSRYAMSWVRQTP 60

QY 61 EKRLVAVATISSGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120
Db 61 EKRLDWAVATISSGGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAMTHCARGV 120

QY 121 DRGAMFEDVWAGTTVTSS 140
Db 121 RRG--YFDVWAGTTVTSS 138

RESULT 2

US-08-579-378A-16
Sequence 16, Application US/08579378A

Patent No. 6210671

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,378A

FILING DATE: 27-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/160,074

FILING DATE: 30-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95112895.8

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8

FILING DATE: 19-SEP-1995

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 79.4%; Score 586.5; DB 3; Length 135;
Best Local Similarity 83.6%; Pred. No. 7.3e-54;
Matches 117; Conservative 9; Mismatches 9; Indels 5; Gaps 3;
QY 1 MNFGSLIFLVYLKGVQCEVVVSGGFFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60

Db 1 MNFGSLIFLVYLKGVQCEVVLVSGGGLVXPGGSLKLSCAAAGFTFSRYAMSWVRQTP 60

QY 61 EKRLVAVATISSGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120
Db 61 EKRLVAVATISSGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAMTHCARGV 120

QY 121 DRGAMFEDVWAGTTVTSS 140
Db 119 D--GYFDVWAGTTVTSS 135

RESULT 3

US-08-379-057-14
Sequence 14, Application US/08379057

Patent No. 5876950

GENERAL INFORMATION:

APPLICANT: Siadak, Anthony W.

APPLICANT: Hollenbaugh, Diane L.

APPLICANT: Gilliland, Lisa K.

APPLICANT: Gordon, Marcia L.

APPLICANT: Bajorath, Jurgen

APPLICANT: Aruffo, Alejandro A.

TITLE OF INVENTION: Monoclonal Antibodies Specific For

TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/379,057

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 32,928

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: ONO133-

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 14

FILING DATE: 19-SEP-1995

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

Query Match 78.6%; Score 581; DB 2; Length 138;
Best Local Similarity 81.4%; Pred. No. 2.8e-53;
Matches 114; Conservative 10; Mismatches 14; Indels 2; Gaps 2;
QY 1 MNFGSLIFLVYLKGVQCEVVVSGGFFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
Db 1 MNGLRILFVLVTLKGVKCEVHLVSGGGLVXPGGSLKLSCAAAGFTFSRYAMSWVRQTP 60
QY 61 EKRLVAVATISSGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120
Db 61 EKRLVAVATISSGGSHHTYPPDSVKGRTISRDNAKNTLYLQMSLSRSEDTAMTHCARGV 120
QY 121 DRGAMFEDVWAGTTVTSS 140
Db 119 D--GYFDVWAGTTVTSS 135

DB 119 DYDSYAMDYMGQSTVTVSS 138

RESULT 4

US-08-976-183A-32
 ; Sequence 32, Application US/08976183A
 ; Patent No. 6307026
 ; GENERAL INFORMATION:
 ; APPLICANT: King, David J.
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Owens, Raymond J.
 ; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
 ; TITLE OF INVENTION: ANTIGEN
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K. Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/976,183A
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/595,848
 ; FILING DATE: 02-FEB-1996
 ; APPLICATION NUMBER: PCT/GB93/02529
 ; FILING DATE: 10-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9225853.2
 ; FILING DATE: 10-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9315249.4
 ; FILING DATE: 22-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bernhard D. Saxe
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 40283/151/CARA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 136 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-976-183A-32

Query Match 76.6%; Score 566; DB 3; Length 136;

Best Local Similarity 78.5%; Pred. No. 1e-51;
 Matches 113; Conservative 8; Mismatches 11; Indels 12; Gaps 2;

QY 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKLSCAAAGFTFSRYAMSWVRQP 60
 DB 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKLSCAAAGFTFSRYAMSWVRQP 60
 QY 61 EKRLWVATISSGSGHTYYPDSVKGRFTISRDNKNTLYLQMSLRSEDTAIYYCAR--- 117
 DB 61 EKRLWVATISSGSGHTYYPDSVKGRFTISRDNKNTLYLQMSLRSEDTAIYYCAR--- 117
 QY 118 -PGYDRGAMFPDVMGAGTIVTVSS 140
 DB 121 VP-----FAWMGGTLTVVSA 136

RESULT 5

US-08-579-378A-20
 ; Sequence 20, Application US/08579378A
 ; Patent No. 6210671
 ; GENERAL INFORMATION:
 ; APPLICANT: Co, Man Sung
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with
 ; TITLE OF INVENTION: L-Selectin
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/579,378A
 ; FILING DATE: 27-DEC-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/160,074
 ; FILING DATE: 30-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/983,946
 ; FILING DATE: 01-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95112895.8
 ; FILING DATE: 17-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95114696.8
 ; FILING DATE: 19-SEP-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Liebschultz, Joe O.
 ; REGISTRATION NUMBER: 37,505
 ; REFERENCE/DOCKET NUMBER: 11823-002220
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 135 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-579-378A-20

Query Match 76.5%; Score 565.5; DB 3; Length 135;

Best Local Similarity 80.7%; Pred. No. 1.2e-51;
 Matches 113; Conservative 10; Mismatches 12; Indels 5; Gaps 3;

QY 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKLSCAAAGFTFSRYAMSWVRQP 60
 DB 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKLSCAAAGFTFSRYAMSWVRQP 60
 QY 61 EKRLWVATISSGSGHTYYPDSVKGRFTISRDNKNTLYLQMSLRSEDTAIYYCARPGY 120
 DB 61 GKGLWVATISSGSGHTYYPDSVKGRFTISRDNKNTLYLQMSLRSEDTAIYYCAR-DY 118
 QY 121 DRGAMFPDVMGAGTIVTVSS 140
 DB 119 D---GVFDYMGQTLTVVSS 135

RESULT 6

US-08-976-183A-34
 ; Sequence 34, Application US/08976183A
 ; Patent No. 6307026

```

; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; City: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-34

Query Match          76.5%; Score 565; DB 3; Length 136;
Best Local Similarity 77.8%; Pred. No. 1,3e-51;
Matches 112; Conservative 9; Mismatches 11; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKVGQCEVVVSSGGGVKPGSLKLSCAAGFTFSRYAMSWVRQT 60
   |||||
DB 1 MNFGSLIFLVYLKVGQCEVVLKVESGGGLVKPGSLKLSCAAGFTFSRYAMSWVRQT 60
   |||||
QY 61 EKLEWVAITSSGGSHTYYPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAR--- 117
   |||||
DB 61 EKLEWVAITSSGGSHTYYPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAPTTV 120
   |||||
QY 118 -PGYDRGAMFEDVWGAGTTVTVSS 140
   |||||
DB 121 VP-----FAYWGGTTLTVSA 136
   |||||

RESULT 7
US-08-976-183A-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
```

```

; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; City: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-33

Query Match          75.8%; Score 560; DB 3; Length 136;
Best Local Similarity 77.8%; Pred. No. 4.4e-51;
Matches 112; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKVGQCEVVVSSGGGVKPGSLKLSCAAGFTFSRYAMSWVRQT 60
   |||||
DB 1 MNFGSLIFLVYLKVGQCEVVLKVESGGGLVKPGSLKLSCAAGFTFSRYAMSWVRQT 60
   |||||
QY 61 EKLEWVAITSSGGSHTYYPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAR--- 117
   |||||
DB 61 EKLEWVAITSSGGSHTYYPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAPTTV 120
   |||||
QY 118 -PGYDRGAMFEDVWGAGTTVTVSS 140
   |||||
DB 121 VP-----FAYWGGTTLTVSA 136
   |||||

RESULT 8
US-08-976-183A-31
; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
```

```

; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/SB93/02529
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CABA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELE: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-31

Query Match          75.6%; Score 559; DB 3; Length 136;
Best Local Similarity 77.1%; Pred. No. 5,6e-51;
Matches 11; Conservative 9; Mismatches 12; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFFVRPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MNFGSLVFLVLLKGVQCEVVLVESGGGLVKGSLKLSCAASGFAFSTYDMSWVRQTP 60

QY 61 EKRLVWATISSGGSHYTPDSVKGKFTISRDNKNTLYLQWSSLRSEDTALYYCAR--- 117
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 EKRLVWATISSGGSHYTPDSVKGKFTISRDNKNTLYLQWSSLRSEDTALYYCAPTV 120

QY 118 -PGYDRGAMFPDVGAGTTVTYSS 140
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 VP-----FAYWGGTLVTYSA 136

RESULT 9
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Holcomb, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallelet, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiser, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrichio Antitumor

```

```

; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match          75.0%; Score 554; DB 1; Length 136;
Best Local Similarity 76.4%; Pred. No. 1.9e-50;
Matches 110; Conservative 9; Mismatches 13; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFFVRPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MNFGSLVFLVLLKGVQCEVVLVESGGGLVKGSLKLSCAASGFAFSTYDMSWVRQTP 60

QY 61 EKRLVWATISSGGSHYTPDSVKGKFTISRDNKNTLYLQWSSLRSEDTALYYCAR--- 117
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 EKRLVWATISSGGSHYTPDSVKGKFTISRDNKNTLYLQWSSLRSEDTALYYCAPTV 120

QY 118 -PGYDRGAMFPDVGAGTTVTYSS 140
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 VP-----FAYWGGTLVTYSA 136

RESULT 10
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Holcomb, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallelet, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiser, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrichio Antitumor
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-57

Query Match 75.0%; Score 554; DB 2; Length 136;
Best Local Similarity 76.4%; Pred. No. 1,9e-50;
Matches 110; Conservative 9; Mismatches 13; Indels 12; Gaps 2;

QY 1 MNFGSLIPVLVVKGVCEVVVSGGFGVFKPGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFGSLIPVLVVKGVCEVVKLVESGGGLVQPGSLKLSCAATSGFTFSDYIMYWRQTP 60
QY 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYCAR--- 117
DB 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYCAPTTV 120
QY 118 -PGYDRCAMFPDYWGAGTTVTVSS 140
DB 121 VP-----FAYWGQGLTVTVSA 136

RESULT 11
US-08-053-171-7
Sequence 7, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co. Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-053-171-7

Query Match 74.7%; Score 552; DB 1; Length 138;
Best Local Similarity 78.6%; Pred. No. 3.1e-50;
Matches 110; Conservative 9; Mismatches 19; Indels 2; Gaps 2;

QY 1 MNFGSLIPVLVVKGVCEVVVSGGFGVFKPGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFGSLIPVLVVKGVCEVVKLVESGGGLVQPGSLKLSCAATSGFTFSDYIMYWRQTP 60
QY 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120
DB 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYHCAR-GM 119
QY 121 DRGAMFPDYWGAGTTVTVSS 140
DB 120 DYGAW-FAYWGQGLTVTVSA 138

RESULT 12
US-08-053-171-11
Sequence 11, Application US/08053171
Patent No. 5562903

GENERAL INFORMATION:
APPLICANT: Co. Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-053-171-11

Query Match 74.7%; Score 552; DB 1; Length 138;
Best Local Similarity 78.6%; Pred. No. 3.1e-50;
Matches 110; Conservative 9; Mismatches 19; Indels 2; Gaps 2;

QY 1 MNFGSLIPVLVVKGVCEVVVSGGFGVFKPGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFGSLIPVLVVKGVCEVVKLVESGGGLVQPGSLKLSCAATSGFTFSDYIMYWRQTP 60
QY 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120
DB 61 EKRLWVATISSGSHHTYPPDSVKGRTTISRDNAKNTLYLQMSLSRSEDTAIYYHCAR-GM 119

```
Qy      121 DRGAFDFDVGAGTIVTSS 140
          ||||| |||||:
Db      120 DYGAW-FAIYWGQGLVTLSA 138
```

RESULT 13
US-08-129-930B-96
; Sequence 96, Application US/08129930B
Date: 08/18/2008

1 GENERAL INFORMATION:
2 APPLICANT: do Couto Dr., Fernando J.R.
3 APPLICANT: Ceriani Dr., Roberto L.
4 APPLICANT: Peterson Dr., Jerry A.
5 APPLICANT: Padian Dr., Eduardo A.
6 TITLE OF INVENTION: Analogue Peptides With Broad
7 Carcinoma Specificity, and Kit and
8 TITLE OF INVENTION: diagnostic Vaccination
9 TITLE OF INVENTION: therapeutic Methods
10 NUMBER OF SEQUENCES: 96
11 CORRESPONDENCE ADDRESS: 96

STREET: 2055 NO. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993

Query Match	73.8%	Score	545.5	DB	1	Length	139	
Best Local Similarity	74.3%	Pred.	No. 1.5e-49					
Matches 104	Conservative	14	Mismatches	21	Indels	1	Gaps	1

Qy 1 MNGGFSILFIPLVLKNGVCEVVNVESGGGFYRPGSLKLSCAAAGFTSRFYMGMWKP 60
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Dd 1 MDGCLSVFLVLLIKGVCEVMVBEGGLVDPGGSLSRLSCAASFATSTAMSMWRQP 60
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 61 EKRLVAVATISGGSGSHYYPDSSVKGRFTISRDNAKNTLYLQMSLRSEDTAIYYCARPGY 120
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Dd 61 GKLEIEMVAETISSGNAYAYQDFTVGRFTISRDNASKNTLYLQNNSLRAEDTAIVYICAREDY 120
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 121 DRGAMPEDVWGACTTVTWS 140
 || || || || || || || || || || || || || || || || || || || || || || || || ||
Dd 121 GRPAM-PAYMGCTLVTS 139
 || || || || || || || || || || || || || || || || || || || || || || || || ||

RESULT 14
US-08-134-346A-51
; Sequence 51, Application US/08134346A
; Patent No. 6281335

```

1  GENERAL INFORMATION:
2  APPLICANT: do Couto, F.J.R.
3  APPLICANT: Ceriani, R.L.C.
4  APPLICANT: Petersen, J.A.
5  TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
6  TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
7  TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
8  NUMBER OF SEQUENCES: 51
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Oestager, Chong & Flaherty
11 STREET: 300 Park Avenue
12 CITY: New York
13 STATE: NY
14 COUNTRY: US
15 ZIP: 10022-7499
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/134,346A
23 FILING DATE: 08-OCT-1993
24 CLASSIFICATION:
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Onofrio, Dara L.
27 REGISTRATION NUMBER: 34,889
28 REFERENCE/DOCKET NUMBER: CIT 149,608
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 212-826-5909
31 TELEFAX: 212-826-5909
32 INFORMATION FOR SEQ ID NO: 51:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 139 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39 US-08-134-346A-51

```

Query Match	73.8%	Score 545.5	DB 3	Length 139
Best Local Similarity	74.3%	Pred. No. 1.5e-49		
Matches 104; Conservative	14;	Mismatches 21;	Indels 1;	Gaps 1

```

QY 1 MNGFSLIFLYLYLVKVOCEVYVYVSGGAFYKPGGSLTSCAAAGFFFSRYAMSWRQTP 60
Db 1 MDGSLVFLVFLYLLKGVOCVQMVYVSGGGLVQPGGSLTSCAAAGFASFYSYAMSWRQAP 60
QY 61 EKLFWATYISGSGSHYYPDSVKRFPTISPRNAGNTLYLQMSLSRSDTAIYCARPGY 120
Db 61 GKGLFWAEIISGSGNAYIYQDTVTGRFTISRNSKNTLYLQMSLSRBDTAIYVCAREDY 120
QY 121 DRGAFPDYWGAGTIVTVYSS 140
Db 121 GIPAW-FAYWGQGTIVTVYSS 139

```

RESULT 15
 US-08-976-288A-96
 ; Sequence 96, Application US/08976288A
 ; Patent No. 631597
 ; GENERAL INFORMATION:
 ; APPLICANT: do Couto Dr., Fernando J.R.
 ; APPLICANT: Ceriani Dr., Roberto L.
 ; APPLICANT: Peterson Dr., Jerry A.
 ; APPLICANT: Padlan Dr., Eduardo A.
 ; TITLE OF INVENTION: Analogue Peptides With Broad
 ; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
 ; TITLE OF INVENTION: Diagnostic Vaccination and
 ; TITLE OF INVENTION: Therapeutic Methods
 ; NUMBER OF SEQUENCES: 96
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder & Poplawski

;
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain of Mab EGPI3F6-1-2 amino acid sequence
US-10-226-795-32

Query Match 74.8%; Score 553; DB 15; Length 158;
Best Local Similarity 76.1%; Pred. No. 6.4e-44;
Matches 108; Conservative 11; Mismatches 21; Indels 2; Gaps 1;
QY 1 MNFGSLIPLVLTGKGVCEVNVVSSGGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
Db 1 MEIQLSWIFPLVLTGKGVCEVNVVSSGGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
QY 61 EKRLVAVATSSGSGSHYTPDSYKGRFTISRDNAKNTLYIQMSLRSEDTAIYCAPPGY 120
Db 61 EKRLVAVATSSGSGSHYTPDSYKGRFTISRDNAKNTLYIQMSLRSEDTAIYCAPPGY 120
QY 121 DRGAMFF--DVGAGTIVTVSS 140
Db 121 YGSSHYAMDYWGQGISVTIVSS 142

Search completed: May 25, 2005, 16:06:49
Job time : 68.7204 secs

מ/צטובב-תערתערררר: תיבת:אגג700

A>Note: the authors translated the codon GAG for residue 117 as Lys
 A>Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are n
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 583.5; DB 2; Length 139;
 Best Local Similarity 82.1%; Pred. No. 7.2e-45;
 Matches 115; Conservative 8; Mismatches 14; Indels 3; Gaps 2;
 QY 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP- 119
 DB 61 EKRLWVATISSRGGT-TYYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP- 119
 QY 120 -YDRGAMFPDVGAGTTVTV 138
 DB 120 YGGYALYGM DYWGQGTSTVTV 139

RESULT 3

Ig heavy chain precursor V region (5-27) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
 C/Accession: C34903
 R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
 J. Biol. Chem. 265, 133-138, 1990
 A/Title: Active site structure and antigen binding properties of idiotypically cross-re
 A/Reference number: A34903; MUID:90094387; PMID:2104617
 A/Accession: C34903
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-142 <BED>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-119/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 578; DB 2; Length 142;
 Best Local Similarity 79.6%; Pred. No. 2.3e-44;
 Matches 113; Conservative 8; Mismatches 19; Indels 2; Gaps 1;
 QY 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 QY 61 EKRLWVATISS-GSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP 118
 DB 61 EKRLWVATISSFGNKPRTGRTYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP 120
 QY 119 GYDRGAMFPDVGAGTTVTVSS 140
 DB 121 GYGGYGFYFAWYWGQGLTVTVSA 142

RESULT 4

Ig heavy chain precursor V region (MAK3) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C/Accession: B26471; S70410
 R/Buckel, P.; Hubner-Parajsz, C.; Matthes, R.; Lenz, H.; Haug, H.; Beaucomp, K.
 Gene 51, 13-19, 1987
 A/Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
 A/Reference number: A91572; MUID:87248058; PMID:3110009
 A/Accession: B26471
 A/Molecule type: mRNA
 A/Residues: 1-152 <BHC>
 A/Cross-references: GB:M16163; NID:g195405; PIDN:AAA3292.1; PID:g195406
 R/Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 172, 1717-1727, 1990

A/Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
 A/Reference number: S70410; MUID:9107975; PMID:2258702
 A/Accession: S70410
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-19 <LEB>
 A/Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

Query Match 77.9%; Score 576; DB 2; Length 152;
 Best Local Similarity 81.0%; Pred. No. 3.7e-44;
 Matches 115; Conservative 5; Mismatches 20; Indels 2; Gaps 1;
 QY 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP- 119
 DB 61 EKRLWVATISSDGSSTYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP- 120
 QY 120 -YDRGAMFPDVGAGTTVTVSS 140
 DB 121 YGNYGDAMDYWGQGTSTVTVSS 142

RESULT 5

Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31666
 R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31666
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-138 <CVI>
 A/Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 542; DB 2; Length 138;
 Best Local Similarity 72.5%; Pred. No. 3.5e-41;
 Matches 103; Conservative 14; Mismatches 19; Indels 6; Gaps 2;
 QY 1 MNFGSLIFLVLTAKVQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MERFGLMFLVLTAKVQCEVQLBSGGGLVPGGSLRLSCAASGFTFSRYAMSWVRQTP 60
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP 118
 DB 61 GKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARP 120
 QY 119 GYDRGAMFPDVGAGTTVTVSS 140
 DB 121 GY---WYFDLWGRGTLTVTVSS 138

RESULT 6

Ig heavy chain precursor V region (5-76) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004

RESULT 14

PL0249

Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0249

R:Shlomchik, M.; Maecelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231, MID:9011618; PMID:2104919

A:Accession: PL0249

A:Molecule type: mRNA

A:Residues: 1-117 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match

70.1%; Score 518; DB 2; Length 117;

Best Local Similarity 83.2%; Pred. No. 4e-39;

Matches 99; Conservative 4; Mismatches 14; Indels 2; Gaps 1;

QY 20 EVVVVSGGGFYKPGGSLKSCAAAGFTFSRYAMSWVROTPEKRLFWATISSGSHYY 79

DB 1 EYLVVSGGGLVYKPGGSLKSCAAGFTFSRYAMSWVROTPEKRLFWANISRGSTYY 60

QY 80 PDSVKGRTISRDNANKTLYLQMSLRSEDTAIYCARPGYDRGAFDPDWGAGTTVTV 138

DB 61 PDSVKGRTISRDNANKTLYLQMSLRSEDTAIYCARPGYDRGAFDPDWGAGTTVTV 117

RESULT 15

S5537

Ig heavy chain V region pe21 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S5537

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
mutations in the variable region genes.

A:Reference number: S5528; MID:95239763; PMID:7536850

A:Accession: S5537

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOE>

A:Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match

70.0%; Score 517; DB 2; Length 120;

Best Local Similarity 83.3%; Pred. No. 5e-39;

Matches 100; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 21 VVVVSGGGFYKPGGSLKSCAAAGFTFSRYAMSWVROTPEKRLFWATISSGSHYY 80

DB 1 VOLQSSGGGLVYKPGGSLKSCAAGFTFSRYAMSWVROTPEKRLFWATISSGSHYY 60

QY 81 DSVKGRFTISRDNANKTLYLQMSLRSEDTAIYCARPGYDRGAFDPDWGAGTTVTV 140

DB 61 DSVKGRFTISRDNANKTLYLQMSLRSEDTAIYCARPGYDRGAFDPDWGAGTTVTV 120

Search completed: May 25, 2005, 16:48:37

Job time : 25.7953 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 68.2419 Seconds

(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773a-4

Perfect score: 739

Sequence: 1 MNFGSLFLVLKGVCE.....DRGAFEDVWGAGTTVSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.5	81.5	487	2	Q99KA4 mus musculus
2	573	77.5	479	2	Q91WPS mus musculus
3	570.5	77.2	196	2	Q65ZL8 mus musculus
4	557	75.4	480	2	Q91XEL mus musculus
5	549	74.3	486	2	Q91Z07 mus musculus
6	532	72.0	117	1	HV58_MOUSE
7	525	71.0	117	1	HV54_MOUSE
8	524	70.9	117	1	HV55_MOUSE
9	523	70.8	117	1	HV59_MOUSE
10	517.5	70.0	606	2	Q6GWT2 mus musculus
11	510	69.0	478	2	Q6P181 mus musculus
12	509.5	68.9	473	2	Q91Z05 mus musculus
13	507.5	68.7	613	2	Q8WUK1 mus musculus
14	507	68.6	470	2	Q6P2A4 mus musculus
15	506	68.5	119	2	Q920E7 mus musculus
16	506	68.5	485	2	Q6PDB8 mus musculus
17	505.5	68.4	475	2	Q6M2Q6 mus musculus
18	504	68.2	464	2	Q6MZU6 mus musculus
19	499	67.5	597	2	Q6GBB9 mus musculus
20	498	67.4	117	1	HV53_MOUSE
21	491.5	66.5	136	1	HV16_MOUSE
22	490	66.3	255	2	Q6KB05 mus musculus
23	489	66.2	493	2	Q6GKX2 mus musculus
24	488.5	66.1	465	2	Q6P6C4 mus musculus
25	488	66.0	487	2	Q80Z17 mus musculus
26	487	65.9	499	2	Q8NSX4 mus musculus
27	477.5	64.6	494	2	Q96K68 mus musculus
28	476.5	64.5	573	2	Q8W338 mus musculus
29	475.5	64.3	473	2	Q6MZV7 mus musculus
30	475	64.3	117	1	HV3C_HUMAN
31	470.5	63.7	487	2	Q6ZVX0 mus musculus

32	468	63.3	472	2	Q6N089 mus musculus
33	466.5	63.1	544	2	Q6P095 mus musculus
34	464.5	62.9	483	2	Q6MZX9 mus musculus
35	464	62.8	493	2	Q8NCL6 mus musculus
36	461.5	62.4	475	2	Q6GKX7 mus musculus
37	460	62.2	466	2	Q6N096 mus musculus
38	458	62.0	466	2	Q6IN78 mus musculus
39	458	62.0	480	2	Q6N094 mus musculus
40	453	61.3	98	1	HV57_MOUSE
41	452.5	61.2	97	1	HV56_MOUSE
42	449.5	60.8	116	1	HV05_CARAU
43	449.5	60.4	519	2	Q6N092 mus musculus
44	444.5	60.1	479	2	Q6MZV6 mus musculus
45	443	59.9	493	2	Q68CN4 mus musculus

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	487 AA.
Q99KA4			
AC Q99KA4			
DT 01-JUN-2001 (TrEMBLrel. 17, Created)			
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE Igh-VJ558 protein.			
CN Name=Igh-VJ558.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC NCBI_Taxid=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CZECH II; TISSUE=Mammary tumor;			
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Scheinfeld Y.S.,			
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,			
RA Jones S.J., Maier M.A.,			
RT "Generation and initial analysis of more than 15,000 full-length human			
and mouse cDNA sequences."			
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=CZECH II; TISSUE=Mammary tumor;			
RA Director MGC Project;			
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL BC004786; AA04786.1; ..			
DR HSSP; P01810; 2P80.			
DR MGD; MGI:96486; Igh-VJ558.			
DR InterPro; IPR007110; I9-like.			
DR InterPro; IPR003597; I9-cl.			
DR InterPro; IPR003006; I9_MHC.			
DR InterPro; IPR003596; I9_v.			
DR Pfam; PF07654; C1-sec; 2.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PS00835; IGV LIKE; 4.			
DR PROSITE; PS00290; IGV_MHC; UNKNOWN 2.			
DR SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;			


```

RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010798; AAH10798.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ
SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
FT
NON TER 1
Query Match 75.4%; Score 557; DB 2; Length 480;
Best Local Similarity 76.3%; Pred. No. 3.5e-48;
Matches 106; Conservative 13; Mismatches 16; Indels 4; Gaps 1;
QY 2 NFGFSLIFLVVLKGVQCEVVVSGGFGVKGSLKSCAAAGTFPSRYAMSWVRQP 61
DB 1 NFGFSLIFLVVLKGVQCEVVVSGGFGVKGSLKSCAAAGTFPSRYAMSWVRQP 60
QY 62 KLELVWATISSGSHYTPDSVKGRFTISRDNANKTLVQLQMSLSRSEDTAIYCARPGYD 121
DB 61 KLELVWATISSGSHYTPDSVKGRFTISRDNANKTLVQLQMSLSRSEDTAIYCARPGYD 119
QY 122 RGAMPFDVWGAGTTVTYSS 140
DB 120 ---WYFDVWGAGTTVTYSS 135

```

```

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH 11; TISSUE=Mammary tumor;
RC Director MGC Project;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010324; AAH10324.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ
SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

```

```

Query Match 74.3%; Score 549; DB 2; Length 486;
Best Local Similarity 74.1%; Pred. No. 2.3e-47;
Matches 106; Conservative 13; Mismatches 20; Indels 4; Gaps 2;
QY 1 NMFGRSLFVLVVLKGVQCEVVVSGGFGVKGSLKSCAAAGTFPSRYAMSWVRQP 60
DB 1 NMFGRSLFVLVVLKGVQCEVVVSGGFGVKGSLKSCAAAGTFPSRYAMSWVRQP 60
QY 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNANKTLVQLQMSLSRSEDTAIYCARPG- 119
DB 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNANKTLVQLQMSLSRSEDTAIYCARPG- 119
QY 120 --YDRGAMPFDVWGAGTTVTYSS 140
DB 120 PLYYSSGYFDSWGGTTITVSS 142

```

RESULT 6

HV58 MOUSE

ID HV58 MOUSE STANDARD; PRT; 117 AA.

AC P18529;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig heavy chain V region 5-76 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/cj;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during the

RT primary immune response.";

RL J. Exp. Med. 169:2007-2019(1989).

CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR; J05056; HVMS57.

DR PDB; 1I81; X-ray; B=20-117.

DR PDB; 1I8K; X-ray; B=20-117.

```

DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 5-76.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78BFA0 CRC64;

Query Match 72.0%; Score 532; DB 1; Length 117;
Best Local Similarity 86.3%; Pred. No. 2,6e-45;
Matches 101; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MNFGFSLIFLVLTAKVQCEVNVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFVLSLIFLALIKGVQCEVHLVSGGGLVKGSGSLKSCVVSGETFNKTAAMSWVRQTP 60

QY 61 EKRLWVAATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117
DB 61 EKRLWVAATISSGGLTYYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117

RESULT 7
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response."
RT J. Exp. Med. 169:2007-2019(1989).
RL -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC PIR; JTO502; HVM834.
DR HSSP; P01810; 2PBJ
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 5-84.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 71.0%; Score 525; DB 1; Length 117;
Best Local Similarity 85.5%; Pred. No. 1,4e-45;
Matches 100; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 1 MNFGFSLIFLVLTAKVQCEVNVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFGLSLIFLVLTAKVCEVNLVSGGGLVKGSGSLKLSCAAAGTFPSRYAMSWVRQTP 60

QY 61 EKRLWVAATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117
DB 61 EKRLWVAATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117

RESULT 8
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response."
RT J. Exp. Med. 169:2007-2019(1989).
RL -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC PIR; JTO502; HVM834.
DR HSSP; P01783; 1IGC.
DR InterPro: IPR007110; Ig-like.
DR HSSP; P01783; 1IGC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 345.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627AC99A CRC64;

Query Match 70.9%; Score 524; DB 1; Length 117;
Best Local Similarity 85.5%; Pred. No. 1,7e-45;
Matches 100; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNFGFSLIFLVLTAKVQCEVNVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWVRQTP 60
DB 1 MNFGLSLIFLVLTAKVCEVNLVSGGGLVKGSGSLKLSCAAAGTFPSRYAMSWVRQTP 60

QY 61 EKRLWVAATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117
DB 61 EKRLWVAATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117

RESULT 9
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CU;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH183 subfamily.
DR PIR; J0507; HWS39.
DR HSSP; P18529; 118K.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 117 Ig heavy chain V region 7-39.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 70.8%; Score 523; DB 1; Length 117;
Best Local Similarity 85.5%; Pred. No. 2, 2e-45;
Matches 100; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
DB 1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 117
DB 61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 117
61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 117

RESULT 10
OG6MY2 PRELIMINARY; PRT; 606 AA.
ID OG6MY2
AC OG6MY2; 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.J., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sec; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; ICG1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;

Query Match 70.0%; Score 517.5; DB 2; Length 606;
Best Local Similarity 66.0%; Pred. No. 4, 8e-44;
Matches 101; Conservative 17; Mismatches 22; Indels 13; Gaps 2;

QY 1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
DB 1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
1 NMFPSLFLVLVKGQCEVVVSGGFFVKGPSGLKLSCAAAGFTFSRYAMSWVRQP 60
61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 119
DB 61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 119
61 EKRLVNAVITSSGSGSHYTPDSVKGFTTSPDNANKTLYLQMSLSRSDTAIYCAR 119
120 -----YDRGAMF---DVGAGTIVTSS 140
DB 121 GAAAGRVVYADYYGMDVGGGTIVTSS 153

RESULT 11
OG6P181 PRELIMINARY; PRT; 478 AA.
ID OG6P181
AC OG6P181; 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.,
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;

Query Match 69.0%; Score 510; DB 2; Length 478;
Best Local Similarity 67.6%; Pred. No. 2,2e-43;
Matches 100; Conservative 13; Mismatches 27; Indels 8; Gaps 1;

QY 1 MNFGSLIFLVYLVKVGQCEVYVVESSGGFVKGSGSLKSCAAAGFTFSRYAMSWRQTP 60
DB 1 MELGSLVFLVVAIEGQCEVQVYVSSGGGLVPGSGSLRLSCAAGFTFSRYAMSWRQAP 60
QY 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDATAYYCARP 118
DB 61 GKLEWVAITSSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDATAYYCARP 120
QY 119 -----GYDRGAMFEDVWGAGTTTVSS 140
DB 121 STMTTANADYYFYMDVWKGKGTIVTSS 148

RESULT 12
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;
RA Strausberg R.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR PIR; S68213; S68213.
DR HSSP; P01783; IIGC.
DR MCD; MGI2144967; AU044919.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 68.9%; Score 509.5; DB 2; Length 473;
Best Local Similarity 70.4%; Pred. No. 2,4e-43;
Matches 100; Conservative 13; Mismatches 22; Indels 7; Gaps 2;

QY 1 MNFGSLIFLVYLVKVGQCEVYVVESSGGFVKGSGSLKSCAAAGFTFSRYAMSWRQTP 60
DB 1 MDSRLNLVFLVLLKVGQCEVQVYVSSGGGLVPGSGSRKLSCAAGFTFDYGNHWROAP 60
QY 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDATAYYCARP 120
DB 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSEDATAYYCARP 118
QY 121 DRGAMF--FDVWGAGTTTVSS 140
DB 119 ---LMLRRIDYWGQGTITVSS 137

RESULT 13
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -.
 DR PIR; F36005; F36005.
 DR PIR; G36005; G36005.
 DR PIR; PH1642; PH1642.
 DR PIR; PH1643; PH1643.
 DR PIR; PH1645; PH1645.
 DR PIR; PH1646; PH1646.
 DR PIR; PL0098; PL0098.
 DR PIR; PL0120; PL0120.
 DR PIR; S15590; S15590.
 DR PIR; S31116; S31116.
 DR PIR; S31119; S31119.
 DR PIR; S70442; S70442.
 DR HSSP; P01861; IADQ.
 DR Pfam; PF07654; C1-secl; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; P550835; IG_LIKE; 5.
 DR PROSITE; P500290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 68.7%; Score 507.5; DB 2; Length 613;
 Best Local Similarity 69.3%; Pred. No. 5.1e-43;

Matches 97; Conservative 16; Mismatches 26; Indels 1; Gaps 1;
 QY 1 MNFGSLIFLVLYLVKGVCEVVVBSGGGFVPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MEGGLSWVFLVALIRGVQCQVLVESGGVGVGPRSLRSLSCAAGFTFSRYAMSWVRQAP 60
 QY 61 EKRLVNAVITSSGGSHYTPDSVKGRFTISRDNKNTLYLQNSLSASEDTAITYCARPGY 120
 DB 61 GKGLEWNAVIAISYDGSNKKYVADSVKGRFTISRDNKNTLYLQNSLSRAEDTAVYYCAK-DW 119
 QY 121 DRGAMPFDVWAGCTTVTVSS 140
 DB 120 SEGVETFDWGGCTVTVSS 139

RESULT 14

Q6PJA4 PRELIMINARY; PRT; 470 AA.
 ID Q6PJA4
 AC Q6PJA4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haileh F.,
 RA Datchenko L., Matrasian K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018747; AAH18747.1; -.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-secl; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR PROSITE; P550835; IG_LIKE; 4.
 DR PROSITE; P500290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 68.6%; Score 507; DB 2; Length 470;
 Best Local Similarity 68.5%; Pred. No. 4.3e-43;

Matches 98; Conservative 13; Mismatches 26; Indels 6; Gaps 2;
 QY 1 MNFGSLIFLVLYLVKGVCEVVVBSGGGFVPGSLKLSCAAAGFTFSRYAMSWVRQTP 60
 DB 1 MEGGLSWVFLVALIRGVQCQVLVESGGVGVGPRSLRSLSCAAGFTFSRYAMSWVRQAP 60
 QY 61 EKRLVNAVITSSGGSHYTPDSVKGRFTISRDNKNTLYLQNSLSASEDTAITYCARPGY 120
 DB 61 GKGLEWNAVIAIKDGGSEKYYVDSVKGRFTISRDNKNTLYLQNSLSRAEDTAVYYCARDG- 119
 QY 121 DRGAMP---FDVWAGCTTVTVSS 140
 DB 120 --SWYRDFDPWGGCTVTVSS 140

RESULT 15

Q920E7 PRELIMINARY; PRT; 119 AA.
 ID Q920E7
 AC Q920E7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotypic heavy chain variable region
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.,
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307937; AAL09421.1; -.
 DR PIR; C25913; C25913.
 DR HSSP; P01783; IIGC.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; P550835; IG_LIKE; 1.
 FT NON TER 1 1
 SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 60.2493 Seconds
(without alignments)
821.675 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

Sequence: 1 MVEFTQIIGLMFWISASRG.....QOSNWPPLFGSGTKLEIKR 128

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16dec04:*

- 1: geneeqp19808:*
- 2: geneeqp19908:*
- 3: geneeqp20008:*
- 4: geneeqp20018:*
- 5: geneeqp20028:*
- 6: geneeqp20038:*
- 7: geneeqp20038:*
- 8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661	100.0	128	ABG74242	Abg74242 Mouse ant
2	634	95.9	127	ABG69687	Abg69687 Murine CM
3	634	95.9	127	AD047787	Ad047787 Mouse CMV
4	622	94.1	127	AAR54093	Aar54093 Sequence
5	619	93.6	127	AAV32405	Aav32405 Mouse ant
6	614	92.9	127	ADF73169	Adf73169 Anti-REL
7	551	83.4	127	AAV32407	Aav32407 Mouse ant
8	534	80.8	108	AAR15438	Aar15438 light cha
9	534	80.8	109	AAR52033	Aar52033 light cha
10	534	80.8	240	AAR15443	Aar15443 single ch
11	533	80.6	107	ADJ80363	Adj80363 Murine an
12	531	80.3	107	ABG69677	Abg69677 Murine CM
13	531	80.3	107	AD047724	Ad047724 Mouse CMV
14	529	80.0	107	ADBS5713	Adbs5713 Human Eph
15	526	79.6	107	AAR38601	Aar38601 HYH light
16	526	79.6	107	AAR58482	Aar58482 Murine HY
17	526	79.6	107	AD101144	Ad101144 Murine mo
18	525	79.4	109	AAV06380	Aav06380 Murine mo
19	524.5	79.3	114	AAAB98665	Aaab98665 Murine pr
20	520	78.7	108	AB027275	Ab027275 Murine 1A
21	518	78.4	108	AAW84094	Aaw84094 Murine VI
22	517	78.2	103	ADM33440	Adm33440 Naide0 VL
23	511	77.3	107	AAW76004	Aaw76004 LM609 ant
24	511	77.3	107	AAAB61362	Aaab61362 Antibody
25	511	77.3	107	AAAG63590	Aaag63590 A light c

26	511	77.3	107	6	AB019800	Ab019800 LM609 1lg
27	511	77.3	107	7	ADG71782	Adg71782 Mab LM609
28	511	77.3	107	8	ADJ57963	Adj57963 Murine LM
29	507	76.7	108	2	AAW00241	Aaw00241 EGF recep
30	507	76.7	159	8	ADL15638	Adl15638 Murine an
31	507	76.7	214	8	ADL15723	Adl15723 Murine an
32	506	76.6	127	2	AAW08945	Aaw08945 Kappa 1lg
33	505	76.6	128	2	AAW30199	Aaw30199 light cha
34	505	76.4	128	5	AAW47724	Aaw47724 light cha
35	503	76.1	123	8	ADL73175	Adl73175 Anti-idio
36	503	76.1	127	2	AAW44176	Aaw44176 Monoclonal
37	494.5	74.8	126	1	AAW90479	Aaw90479 Chimeric
38	494	74.7	159	8	ADL15664	Adl15664 Partial m
39	493	74.6	127	2	AAW08941	Aaw08941 Kappa 1lg
40	493	74.6	109	2	AAW89176	Aaw89176 Anti-p53
41	492.5	74.5	109	2	AAW89176	Aaw89176 Anti-p53
42	492	74.4	259	3	AAW09775	Aaw09775 TWV 30K m
43	492	74.4	264	7	ADD25839	Add25839 Binding d
44	492	74.4	548	7	ADD25711	Add25711 Binding d
45	487	73.7	127	7	ADD25703	Add25703 Binding d

ALIGNMENTS

RESULT 1	ABG74242	standard, protein, 128 AA.
AC	ABG74242	
XX	XX	
XX	XX	
DT	22-APR-2003	(first entry)
DE	Mouse antibody MB3.6 light chain variable region.	
XX	XX	
KW	T-cell receptor; cytostatic; dermatological; neuroprotective;	
KW	immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;	
KW	3E11; prostate-specific membrane antigen; zeta signalling chain;	
KW	CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;	
KW	small cell lung cancer; light chain variable region; mouse.	
OS	Mus sp.	
PN	US2002132983-A1.	
XX	XX	
PD	19-SEP-2002.	
XX	XX	
PR	30-NOV-2000; 2000US-0250087P.	
PR	30-NOV-2000; 2000US-0250089P.	
XX	XX	
PA	(JUNG/) JUNGHANS R P.	
PI	Junghans R P.	
XX	XX	
DR	WPI; 2003-208946/20.	
DR	N-PSDB; ABX16567.	
PT	New chimeric nucleotide useful in treating patients with disorders, such as	
PT	melanoma, neuroendocrine disorders, prostate and small cell lung cancer	
PT	comprises GD3 and/or PSMA binding domains of antibody.	
XX	XX	
PS	Disclosure; Page 10-11; 35pp; English.	
CC	The invention relates to a chimeric molecule comprising the GD3	
CC	(ganglioside antigen) binding domain of antibody MB3.6, with any of 3	
CC	variable gene sequences, or the PSMA (prostate-specific membrane antigen)	
CC	binding domain of antibody 3D8, 4D4 and 3E11, with variable gene	
CC	sequences, the zeta signalling chain of the T cell receptor and an	
CC	intervening CD8alpha hinge in which cysteine residues have been mutated.	
CC	The chimeric molecules expressed in T cells or NK cells or other	
CC	effector cells are useful in treating patients with cancers expressing	

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody MB3.6 light chain variable region
XX

XX Sequence 128 AA;

Query Match 100.0%; Score 661; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVEFTPOLGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
DB 1 MVEFTPOLGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
QY 61 HESPRLLIKYASQISGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQOQNSWPLTFGS 120
DB 61 HESPRLLIKYASQISGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQOQNSWPLTFGS 120
QY 121 GTKLEIRK 128
DB 121 GTKLEIRK 128

RESULT 2

AAB69687
ID AAB69687 standard; protein; 127 AA.

XX AAB69687;
DT 30-APR-2001 (first entry)

XX Murine CMV5 antibody light chain SEQ ID NO: 83.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KM light chain; graft versus host disease; transplant; autoimmune disease;
KM multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KM myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

XX US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-00484537.

XX 28-DEC-1988; 88US-00290975.

XX 13-FEB-1989; 89US-00310252.

XX 28-SEP-1990; 90US-00590274.

XX 19-DEC-1990; 90US-00634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen CL, Selick HE;

XX WPI, 2001-190856/19.

XX N-PSDB; AAF58747.

XX Producing humanized immunoglobulin, involves producing a cell containing
PT DNA segments encoding humanized heavy and light chain variable regions,
PT and expressing the DNA segments in the cell.

XX Example 8; Fig 39; 145pp; English.

XX The present invention describes a method of producing humanised
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a
CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of graft-versus-

CC host disease, transplant rejection, autoimmune diseases such as diabetes,
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
CC leukemia. The present sequence is an antibody used to demonstrate the
CC method of the invention
XX

XX Sequence 127 AA;

Query Match 95.9%; Score 634; DB 4; Length 127;
Best Local Similarity 96.1%; Pred. No. 6.3e-38;
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVEFTPOLGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
DB 1 MVEFTPOLGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
QY 61 HESPRLLIKYASQISGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQOQNSWPLTFGS 120
DB 61 HESPRLLIKYASQISGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQOQNSWPLTFGS 120
QY 121 GTKLEIRK 127
DB 121 GTKLEIRK 127

RESULT 3

ADO47787
ID ADO47787 standard; protein; 127 AA.

XX ADO47787;

XX 15-JUL-2004 (first entry)

XX Mouse CMV5 antibody light chain variable region #2.

XX humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;
KM donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;
KM IL-2 receptor; T-cell mediated disorder; mouse; CMV5 antibody;
KM light chain variable region.

XX Mus sp.

XX US2004058414-A1.

XX 25-MAR-2004.

XX 30-MAY-2003; 2003US-00452357.

XX 28-DEC-1988; 88US-00290975.

XX 13-FEB-1989; 89US-00310252.

XX 28-SEP-1990; 90US-00590274.

XX 07-JUN-1995; 95US-00484537.

XX 22-NOV-2000; 2000US-00718993.

XX (QUEB/) QUEEN C L.

XX (COMS/) CO M S.

XX (SCHN/) SCHNEIDER W P.

XX (LAND/) LANDOLFI N F.

XX (COEL/) COELINGH K L.

XX (SELI/) SELICK H E.

XX Queen CL, Co MS, Schneider WP, Landolfi NF, Coelinhg KL;

XX Selick HE;
XX WPI, 2004-304235/28.
XX N-PSDB; ADO47786.
XX Designing humanized immunoglobulin chain comprises substituting human
PT framework amino acids of acceptor immunoglobulin with corresponding amino
PT acid from donor immunoglobulin at position in immunoglobulin.
XX Disclosure; Fig 48; 130pp; English.

CC The invention describes a method of designing a humanised immunoglobulin
 CC (19) chain. The method comprises substituting human framework amino acids
 CC of the acceptor Ig with a corresponding amino acid from the donor Ig at a
 CC position in the Ig, where the amino acid is immediately adjacent to one
 CC of the CDR's or the amino acid is predicted to have a side chain atom
 CC whose Van der Waals surface is 3 angstroms from the CDR's in three-
 CC dimensional Ig model and is capable of interacting with the antigen or
 CC with the CDR's of the humanised Ig that when the chain is a heavy chain,
 CC substituted amino acid(s) is capable of interacting with CDR's 2 or 3.
 CC Also described are: an Ig comprising two light/heavy chains; a DNA
 CC sequence which upon expression encodes a humanised Ig chain; a
 CC polynucleotide composition comprising a DNA sequence coding for a
 CC humanised Ig; a composition comprising a pure humanised immunoglobulin
 CC capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL
 CC -2 receptor; treating T-cell mediated disorders in a human patient
 CC comprising administering to the patient a therapeutic dose of an Ig; and
 CC a composition comprising a pure humanised Ig reactive with the p75 chain
 CC of the human IL-2 receptor. The method is used for designing a humanised
 CC immunoglobulin chain, useful for treating T-cell mediated disorders in a
 CC human patient. The invented method produces an Ig chain that is easily
 CC and economically produced. This is the amino acid sequence of mouse CMV5
 CC antibody light chain variable region. Residues in the human antibody
 CC framework can be replaced with residues from the mouse antibody to create
 CC a humanised antibody.
 CC
 SQ Sequence 127 AA;
 Query Match 95.9%; Score 634; DB 8; Length 127;
 Best Local Similarity 96.1%; Pred. No. 6,3e-38;
 Matches 122; Conservative 1; Mismatches 0; Gaps 0;
 QY 1 MVTFTQILGLMFWISASRGDIVLQSPATLSVTGDSVSLSCRASQISNNLHWYQOKS 60
 DB 1 MVTFTQILGLMFWISASRGDIVLQSPATLSVTGDSVSLSCRASQISNNLHWYQOKS 60
 QY 61 HESPRLLIKYASQISIGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPTFGS 120
 DB 61 HESPRLLIKYASQISIGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPTFGS 120
 QY 121 GTKLBIK 127
 DB 121 GTKLBIK 127
 DB 121 GTKLBIK 127
 RESULT 4
 AAR54093 standard; protein; 127 AA.
 AAR54093;
 XX 25-MAR-2003 (revised)
 DT 29-DEC-1994 (first entry)
 XX
 DE Sequence of mouse V-kappa showing the sequences of recombinant anti-FHV-1
 DE antibody CDRs 1, 2 and 3.
 XX
 KM Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KM complementarity determining region.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= leader
 FT Region 21..43
 FT /label= FR1
 FT Region 44..54
 FT /label= CDR1
 FT Region 55..70
 FT /label= FR2
 FT Region 71..76
 FT /label= CDR2
 FT Region 77..108

FT /label= FR3
 FT Region 109..117
 FT /label= CDR3
 FT Region 118..127
 FT /label= FR4
 FT
 PN MO9412661-A1.
 XX
 PD 09-JUN-1994.
 XX
 XX 25-NOV-1993; 93WO-JP001724.
 PF
 PR 28-NOV-1992; 92JP-00341255.
 XX
 PA (KAGA) CHEMA SERO THERAPEUTIC RES INST.
 XX
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 DR WPI; 1994-200288/24.
 DR N-PSDB; AA064167.
 XX
 XX
 PT Feline monoclonal antibody and recombinant antibodies specific for FHV-1
 PT - for detection, treatment and prevention of FHV-1 infection.
 PS Disclosure; Page 18-19; 53pp; Japanese.
 CC The inventors claim a monoclonal antibody against feline herpes virus
 CC (FHV-1). They also claim a recombinant antibody against FHV-1 and
 CC fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are used in the
 CC detection, treatment and prevention of FHV-1. The sequences of the CDRs
 CC in the VH of the recombinant anti-FHV-1 antibody are given in AAR54092.
 CC The sequences of the CDRs in the VL of the recombinant anti-FHV-1
 CC antibody are given in AAR54093. These CDR sequences are claimed. (Updated
 CC on 25-MAR-2003 to correct PW field.)
 CC
 SQ Sequence 127 AA;
 Query Match 94.1%; Score 622; DB 2; Length 127;
 Best Local Similarity 94.5%; Pred. No. 4,5e-37;
 Matches 120; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVTFTQILGLMFWISASRGDIVLQSPATLSVTGDSVSLSCRASQISNNLHWYQOKS 60
 DB 1 MVTFTQILGLMFWISASRGDIVLQSPATLSVTGDSVSLSCRASQISNNLHWYQOKS 60
 QY 61 HESPRLLIKYASQISIGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPTFGS 120
 DB 61 HESPRLLIKYASQISIGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPTFGS 120
 QY 121 GTKLBIK 127
 DB 121 GTKLBIK 127
 DB 121 GTKLBIK 127
 RESULT 5
 AAY32405 standard; protein; 127 AA.
 AAY32405;
 XX
 AC AAY32405;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Mouse anti-verotoxin II antibody VTm1-1 light chain variable region.
 XX
 KM Verotoxin II; VT2; shiga-like toxin; VTm1-1; MvVTm1-1;
 KM monoclonal antibody; light chain; mouse; humanised antibody;
 KM Escherichia coli; VTBC; infection; haemolytic uraemic syndrome; HUS;
 KM therapy.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..20

FT /note= "signal peptide"
 FT Protein 21..127
 FT /note= "mature protein"
 FT Region 44..54
 FT /note= "complementarity determining region 1"
 FT Misc-difference 62
 FT /note= "encoded by GAG"
 FT Region 70..76
 FT /note= "complementarity determining region 2"
 FT Region 109..117
 FT /note= "complementarity determining region 3"
 XX
 XX WO9595629-A1.
 XX
 XX 25-NOV-1999.
 XX
 XX 19-MAY-1999; 99MO-US011179.
 XX
 XX 20-MAY-1998; 98US-0086570P.
 XX
 XX (TEIJU) TEIJUN LTD.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M,
 XX WPI; 2000-086580/07.
 XX DR N-PSDB; AAY35242.
 XX
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli.
 XX
 XX Claim 5; Fig 1b; 59pp; English.
 XX
 CC This sequence represents the light chain variable region of murine
 CC monoclonal antibody Vtm1-1 (Muvtm1-1), an antibody that specifically
 CC binds to the B subunit of verotoxin II (VT2). The invention relates to
 CC humanised antibodies against VT2 that are capable of neutralizing VT2
 CC and/or VT2 variants. The humanised antibody is a humanized form of Muvtm1
 CC -1 comprising the complementarity determining regions of Muvtm1-1 and the
 CC heavy and light chain variable region frameworks from the human GP4
 CC antibody heavy and light chain frameworks, provided that at least 1
 CC position selected from L49, H29, H30, H49 and H98 is occupied by the
 CC amino acid at the equivalent position of the Muvtm1-1 antibody heavy or
 CC light chain variable region framework. Such humanized antibodies (see
 CC AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times that of
 CC Muvtm1-1. They are used for treating a patient suffering from, or at risk
 CC of, the toxic effects from VT2 (claimed), especially for treating
 CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic
 CC uraemic syndrome (HUS)
 CC
 CC Sequence 127 AA:
 SQ
 Query Match 93.6%; Score 619; DB 3; Length 127;
 Best Local Similarity 93.7%; Pred. No. 7,4e-37;
 Matches 119; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVTFTPOLIGLMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGSAQIISNNLHWYQOKS 60
 DB 1 MVTFTPOLIGLMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGSAQIISNNLHWYQOKS 60
 QY 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLTINSVETEDFGMYFCQOQSNWPLTFGS 120
 DB 1 MVTFTPOLIGLMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGSAQIISNNLHWYQOKS 60
 QY 121 GTKLEIK 127
 DB 121 GTKLEIK 127

AC ADF73169;
 XX
 XX 26-FEB-2004 (first entry)
 XX
 DE Anti-RELp fusion antibody CMO 338 LC variable region SEQ ID NO:28.
 XX
 XX anti-RELp fusion antibody; RELp fusion antibody; cytotaxtic;
 KW cardiovascular; immunomodulator; neuroprotective; nootropic;
 KW gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disorder; human.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX WO2003102017-A2.
 XX
 XX 11-DEC-2003.
 XX
 XX 02-JUN-2003; 2003MO-US017357.
 XX
 XX 03-JUN-2002; 2002US-0385305P.
 XX
 XX (CENZ) CENTOCOR INC.
 XX
 XX Carton J, Giles-Komar J, Scallion B, Sraquet K,
 XX WPI; 2004-053426/05.
 XX DR N-PSDB; ADF73179.
 XX
 XX New mammalian Reg like protein (RELp) fusion antibody, useful for
 PT preparing a composition for diagnosing or treating a RELp protein-related
 PT condition in a cell, tissue, organ or animal, e.g., cancer.
 XX
 XX Claim 4; SEQ ID NO 28; 78pp; English.
 XX
 CC The present invention describes a mammalian anti-RELp fusion antibody (1)
 CC which comprises: (a) at least one heavy chain variable region comprising
 CC ADF73148 or ADF73168 and at least one light chain variable region
 CC comprising ADF73149, ADF73169 or ADF73180; or (b) all of the
 CC complementarity determining regions (CDRs) of ADF73142 to ADF73147 or
 CC ADF73162 to ADF73167. Also described: (1) a pharmaceutical composition
 CC comprising the mammalian RELp fusion antibody and at a carrier or diluent
 CC ; (2) an isolated nucleic acid encoding the mammalian RELp fusion
 CC antibody; (3) an isolated nucleic acid vector comprising the isolated
 CC nucleic acid; (4) a prokaryotic or eukaryotic host cell comprising the
 CC isolated nucleic acid; (5) a method for producing at least one RELp
 CC fusion antibody; (6) a method for diagnosing or treating a RELp protein-
 CC related condition in a cell, tissue, organ or animal; (7) an article of
 CC manufacture for human pharmaceutical or diagnostic use, comprising
 CC packaging material and a container comprising a solution or a lyophilised
 CC form of the mammalian RELp fusion antibody; and (8) a medical device,
 CC comprising the isolated mammalian RELp fusion antibody, where the device
 CC is suitable to contacting or administering the at least one RELp fusion
 CC antibody. (1) has cytostatic, cardiovascular, immunomodulator,
 CC neuroprotective and nootropic activities, and can be used in gene
 CC therapy. The mammalian RELp fusion antibody is useful for preparing a
 CC composition for diagnosing or treating a RELp protein-related condition
 CC in a cell, tissue, organ or animal, e.g., cancer, immune disorders,
 CC cardiovascular and neurological disorders. The present sequence is used
 CC in the exemplification of the present invention.
 CC
 CC Sequence 127 AA:
 SQ
 Query Match 92.9%; Score 614; DB 8; Length 127;
 Best Local Similarity 91.3%; Pred. No. 1.7e-36;
 Matches 116; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVTFTPOLIGLMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGSAQIISNNLHWYQOKS 60
 DB 1 MVTFTPOLIGLMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGSAQIISNNLHWYQOKS 60
 QY 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLTINSVETEDFGMYFCQOQSNWPLTFGS 120

Db 61 HGPSRLIKYASQSIGIPRFGSGSGTDFLTINNVEDFGLYFCQOQNSWPLTFGA 120
 QY 121 GTRLEIK 127
 Db 121 GTRLEIK 127

RESULT 7
 AAY32407
 ID AAY32407 standard; protein; 127 AA.
 XX
 AC AAY32407;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE Mouse anti-verotoxin II antibody VTm1-1 humanised VL region.
 XX
 KW Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1;
 KW monoclonal antibody; light chain; mouse; humanised antibody; human;
 KW Escherichia coli; VTBC; infection; haemolytic uraemic syndrome; HUS;
 KW therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 "signal peptide"
 FT Protein 21..127
 FT /note= "mature protein"
 FT Region 44..54
 FT /note= "complementarily determining region 1"
 FT Region 70..76 "complementarily determining region 2"
 FT /note= "complementarily determining region 2"
 FT Region 109..117
 FT /note= "complementarily determining region 3"
 XX
 PN WO959629-A1.
 PD 25-NOV-1999.
 XX
 PF 19-MAY-1999; 99WC-US011179.
 XX
 PR 20-MAY-1998; 98US-0086570P.
 XX
 PA (TEJU) TEJUIN LTD.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
 XX WPI; 2000-086580/07.
 DR N-PSDB; AA235244.
 XX
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli.
 PS
 PS Claim 12; Fig 2b; 59pp; English.

This sequence represents a humanised light chain variable region of murine monoclonal antibody VTm1-1 (MuVTm1-1), an antibody that specifically binds to the B subunit of verotoxin II (VT2). The invention relates to humanised antibodies against VT2 that are capable of neutralizing VT2 and/or VT2 variants. The humanised antibody is a humanized form of MuVTm1-1 comprising the complementarily determining regions of MuVTm1-1 and the heavy and light chain variable region frameworks from the human GF4 antibody heavy and light chain frameworks, provided that at least 1 position selected from 149, H29, H30, H49 and H98 is occupied by the amino acid at the equivalent position of the MuVTm1-1 antibody heavy or light chain variable region framework. Such humanized antibodies have an affinity for VT2 that is 3-, 5 or 10-times that of MuVTm1-1. They are used for treating a patient suffering from, or at risk of, the toxic effects from VT2 (claimed), especially for treating verotoxin producing Escherichia coli (VTBC) infection, and haemolytic

CC uraemic syndrome (HUS)
 XX
 SQ Sequence 127 AA;
 XX

Query Match 83.4%; Score 551; DB 3; Length 127;
 Best Local Similarity 81.9%; Pred. No. 5.2e-32;
 Matches 104; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 MFTPOIIGLMFWISASRGDVLNOSPATLSVTPGDSVSLSCRASQITSNLHWYQOKS 60
 |||||
 Db 1 MFTPOIIGLMFWISASRGELVLTQSPATLSVSPERATLSCRASQITSNLHWYQOKP 60
 |||||

QY 61 HGPSRLIKYASQSIGIPRFGSGSGTDFLTINSVETBDFGMVFCQOQNSWPLTFGS 120
 :|||
 Db 61 GQAPRLIKSASQSIGIPARFSGSGTDFLTITISLESDFAYYCCQSYSWPLTFQ 120
 |||||

QY 121 GTRLEIK 127
 |||||
 Db 121 GTRLEIK 127

RESULT 8
 AAR15438
 ID AAR15438 standard; protein; 108 AA.
 XX
 AC AAR15438;
 XX
 DT 25-FEB-1992 (first entry)
 XX
 DE Light chain variable region of Mab 1A6.
 XX
 KW HRV; ICAW-1; antigen-binding fragment; inflammation; auto-immune disease.
 XX
 OS Homo sapiens.
 XX
 PN EP459577-A.
 PD 04-DEC-1991.
 XX
 PF 25-MAY-1991; 91EP-00201243.
 XX
 PR 01-JUN-1990; 90US-00532001.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Colunno RJ, Condra JH, Tomassini JE, Sardana VV;
 XX WPI; 1991-355850/49.
 DR
 XX
 PT Microbially expressed portions of monoclonal antibody - can block
 PT attachment of rhinovirus ligands to inter-cellular adhesion molecule
 PT (ICAM-1).
 XX
 PS Claim 1; Page 19; 28pp; English.

This is one of six antibody fragments from Mab's specific for domain 1 of ICAM-1. Mab 1A6 also specifically blocks the major group of human rhinovirus from binding to and infecting HeLa cells. The peptide fragments can be used to treat or prevent rhinovirus infection. See AAR15437-R15443

SQ Sequence 108 AA;
 XX

Query Match 80.8%; Score 534; DB 2; Length 108;
 Best Local Similarity 95.4%; Pred. No. 7.3e-31;
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLQSPATLSVTPGDSVSLSCRASQITSNLHWYQOKSHSPRLIKYASQSIGIPS 80
 |||||
 Db 1 DIVLQSPATLSVTPGDSVSLSCRASQISNNLHWYQOKSHSPRLIKYASQSIGIPS 60
 |||||

QY 81 RFGSGSGTDFLTINSVETBDFGMVFCQOQNSWPLTFSGGTRLEIKR 128
 |||||

Db 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNMPTFGGTYLTIKR 108

RESULT 9

AAAR52033 standard; protein; 109 AA.

AC AAR52033;

DT 26-SEP-1996 (first entry)

XX Light chain variable region of murine antibody 3HfM.

XX antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
XX modelling; surface residue; modify.

OS Mus sp.

XX Key Location/Qualifiers

FT Region 1..23

FT /label= framework_region_1

FT /note= "FR 1"

FT Region 24..34

FT /label= complementarity_determining_region_1

FT /note= "CDR 1"

FT Region 35..49

FT /label= FR_2

FT 50..56

FT /label= CDR_2

FT 57..88

FT /label= FR_3

FT 89..97

FT /label= CDR_3

FT 98..109

FT /label= FR_4

XX EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-00307051.

XX 09-SEP-1992; 92US-00942245.

XX (IMMU-) IMMUNOGEN INC.

XX PI Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;

XX WPI; 1994-120230/15.

XX Method of resurfacing of rodent antibodies to produce humanised antibody
PT forms - for producing non human antibodies with improved therapeutic
PT efficiency by presenting human surface on V-region.

XX Example 1; Fig 3A; 230p; English.

XX The present sequence is that of the light chain variable (LC VR) region
CC of murine antibody 3HfM. This sequence was aligned with 11 other known
CC antibody LC VRs and a set of framework positions of surface exposed amino
CC acid residues was determined. This information can be used in a method to
CC determine how to modify a rodent antibody or fragment by resurfacing in
CC order to produce a humanised rodent antibody. Residues (determined from
CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC combinations of surface residues in the murine sequences were found in
CC the human sequences and vice versa. However the residues in individual
CC positions appear to be conserved

XX Sequence 109 AA;

XX Query Match 80.8%; Score 534; DB 2; Length 109;
XX Best Local Similarity 95.4%; Pred. No. 7,4e-31;

Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQQKSHESPRLLIKYASQISGIPS 80

Db 1 DIVLTQSPATLSVTPGDVSVLSCRASQISNNLHWYQQKSHESPRLLIKYASQISGIPS 60

QY 81 RFGSGSGTDFTLINSVETEDFGMFCCQSNMPTFGGTYLTIKR 128

Db 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNMPTFGGTYLTIKR 108

RESULT 10

AAAR15443 standard; protein; 240 AA.

AC AAR15443;

DT 25-FEB-1992 (first entry)

XX Single chain Fv from pSCV1 for blocking HRV binding to ICAM-1.

XX antigen-binding fragment; inflammation; auto-immune disease.

XX Homo. sapiens.

XX EP459577-A.

XX 04-DEC-1991.

XX 25-MAY-1991; 91EP-00201243.

XX 01-JUN-1990; 90US-00532001.

XX (MERI) MERCK & CO INC.

XX PI Colombo RJ, Condra JH, Tomassini JE, Sardana VV;

XX WPI; 1991-355850/49.

XX Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion molecule
PT (ICAM-1).

XX Claim 5; Page 21; 28pp; English.

XX The Fv fragment encoded by pSCV1 was able to protect cells against
CC infection by HRV-14. It was less active than modified Fv fragments which
CC included a Gly-Gly-Gly-ser flexible linker between the L and H chains
CC as either a monomer or a dimer. See also AAR15437-R15442

XX Sequence 240 AA;

XX Query Match 80.8%; Score 534; DB 2; Length 240;
XX Best Local Similarity 95.4%; Pred. No. 1.5e-30; Indels 0; Gaps 0;
XX Matches 103; Conservative 2; Mismatches 3;

QY 21 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQQKSHESPRLLIKYASQISGIPS 80

Db 1 DIVLTQSPATLSVTPGDVSVLSCRASQISNNLHWYQQKSHESPRLLIKYASQISGIPS 60

QY 81 RFGSGSGTDFTLINSVETEDFGMFCCQSNMPTFGGTYLTIKR 128

Db 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNMPTFGGTYLTIKR 108

RESULT 11

ADJ80363 standard; protein; 107 AA.

AC ADJ80363;

DT 06-MAY-2004 (first entry)

DE Murine anti-human mannose binding lectin antibody variable light chain.
 XX
 KM hybrid antibody; antibody; framework region; homology; immunogenicity.
 XX
 OS Mus sp.
 XX WO2003048321-A2.
 XX
 PN 12-JUN-2003.
 PD
 XX 03-DEC-2002; 2002WO-US038450.
 XX
 PF 03-DEC-2001; 2001US-0336591P.
 XX
 PR (ALEX-) ALEXION PHARM INC.
 XX
 PA Rother R, Wu D;
 XX
 PI WPI; 2003-513753/48.
 XX
 DR
 XX
 XX
 PT Producing a hybrid antibody or hybrid antibody fragment by operatively
 PT linking the selected framework sequences to one or more complementarity
 PT determining regions of the initial antibody.
 PS
 XX Example 1; SEQ ID NO 123; 77pp; English.

CC The invention relates to a method of producing a hybrid antibody or
 CC hybrid antibody fragment by: (i) providing an initial antibody having
 CC specificity for a target; (ii) determining the sequence of a variable
 CC region of the initial antibody; (iii) selecting a first component of the
 CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
 CC sequence of the first component to sequences contained in a reference
 CC database of antibody sequences or antibody fragment sequences from a
 CC target species; (v) selecting a sequence from an antibody in the database
 CC which demonstrates a high degree of homology to the first component; (vi)
 CC selecting a second component of the variable region which is different
 CC than the first component, the second component selected from the group
 CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
 CC second component to sequences contained in a reference database of
 CC antibody sequences or antibody fragment sequences from the target species
 CC; (viii) selecting a sequence from the database which demonstrates a high
 CC degree of homology to the second component and which is from a different
 CC antibody than the selected antibody; and (ix) operatively linking the
 CC selected framework sequences to one or more complementarity determining
 CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
 CC hybrid antibody fragment. The method is useful for producing a hybrid
 CC antibody or hybrid antibody fragment (claimed). The antibody and
 CC fragments are useful for therapeutic and diagnostic purposes. The method
 CC uses entire framework regions from a single antibody variable heavy or
 CC are highly homologous and exhibit reduced immunogenicity while
 CC maintaining an optimum binding profile. This sequence represents the
 CC amino acid sequence of an initial murine anti-human mannose binding
 CC lectin antibody light chain used to generate the hybrid antibodies of the
 CC invention.

XX
 SQ Sequence 107 AA;

Query Match 80.6%; Score 533; DB 7; Length 107;
 Best Local Similarity 96.3%; Pred. No. 8.6e-31;

Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNILHWYQOKSHSPRLILTKYASQISIGIPS 80
 DB 1 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNILHWYQOKSHSPRLILTKYASQISIGIPS 60
 QY 81 RFGSGSGGTFDFTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
 DB 61 RFGSGSGGTFDFTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 107

RESULT 12
 AAB69677

ID AAB69677 standard; protein; 107 AA.

XX
 AC AAB69677;

XX
 DT 30-APR-2001 (first entry)

XX
 DE Murine CMV5 antibody light chain SEQ ID NO: 62.

XX
 KM Humanised immunoglobulin, mouse; human; antibody; heavy chain; diabetes;
 KM light chain; graft versus host disease; transplant; autoimmune disease;
 KM multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KM myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX
 OS Mus sp.

XX
 PN US6180370-B1.

XX
 PD 30-JAN-2001.

XX
 PF 07-JUN-1995; 95US-00484537.

XX
 PR 28-DEC-1988; 88US-00290975.

XX
 PR 13-FEB-1989; 89US-00310252.

XX
 PR 28-SEP-1990; 90US-00590274.

XX
 PR 19-DEC-1990; 90US-00634278.

XX
 PA (PROT-) PROTEIN DESIGN LABS INC.

XX
 PI Queen CL, Selick HE;

XX
 DR WPI; 2001-190856/19.

XX
 PT Producing humanized immunoglobulin, involves producing a cell containing
 PT DNA segments encoding humanized heavy and light chain variable regions,
 PT and expressing the DNA segments in the cell.

XX
 PS Disclosure; Fig 6; 145pp; English.

CC The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of graft-versus-
 CC host disease, transplant rejection, autoimmune diseases such as diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
 CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
 CC leukemia. The present sequence is an antibody used to demonstrate the
 CC method of the invention

XX
 SQ Sequence 107 AA;

Query Match 80.3%; Score 531; DB 4; Length 107;
 Best Local Similarity 95.3%; Pred. No. 1.2e-30;

Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNILHWYQOKSHSPRLILTKYASQISIGIPS 80
 DB 1 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNILHWYQOKSHSPRLILTKYASQISIGIPS 60
 QY 81 RFGSGSGGTFDFTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
 DB 61 RFGSGSGGTFDFTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 107

RESULT 13

AD047724
 AD047724 standard; protein; 107 AA.

XX
 AC AD047724;

XX
 DT 15-JUL-2004 (first entry)

XX
 DE Mouse CMV5 antibody light chain variable region #1.

XX humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;
 KW donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;
 KM IL-2 receptor; T-cell mediated disorder; mouse; CMV5 antibody;
 KM light chain variable region.

XX Mus sp.

XX US2004058414-A1.

XX 25-MAR-2004.

XX 30-MAY-2003; 2003US-00452357.

XX 28-DEC-1988; 88US-00290975.

XX 13-FEB-1989; 89US-00310252.

XX 28-SEP-1990; 90US-00590274.

XX 07-JUN-1995; 95US-00484537.

XX 22-NOV-2000; 2000US-00718993.

XX (QUEE/) QUEEN C L.

XX (COMS/) CO M S.

XX (SCHN/) SCHNEIDER W P.

XX (LAND/) LANDOLFI N F.

XX (COEL/) COELLINGH K L.

XX (SEL1/) SELICK H E.

XX Queen CL, Co MS, Schneider WP, Landolffi NF, Coellingh KL,
 PI Selick HE;

XX WPI; 2004-304235/28.

XX Designing humanized immunoglobulin chain comprises substituting human
 PT framework amino acids of acceptor immunoglobulin with corresponding amino
 PT acid from donor immunoglobulin at position in immunoglobulin.

XX Example 3; Fig 6; 130pp; English.

XX The invention describes a method of designing a humanised immunoglobulin
 CC (Ig) chain. The method comprises substituting human framework amino acids
 CC of the acceptor Ig with a corresponding amino acid from the donor Ig at a
 CC position in the Ig, where the amino acid is immediately adjacent to one
 CC of the CDR's or the amino acid is predicted to have a side chain atom
 CC whose Van der Waals surface is 3 angstroms from the CDR's in three-
 CC dimensional Ig model and is capable of interacting with the antigen or
 CC with the CDR's of the humanised Ig that when the chain is a heavy chain,
 CC substituted amino acid(s) is capable of interacting with CDR's 2 or 3.

CC Also described are: an Ig comprising two light/heavy chains; a DNA
 CC sequence which upon expression encodes a humanised Ig chain; a
 CC polynucleotide composition comprising a DNA sequence coding for a
 CC humanised Ig; a composition comprising a pure humanised immunoglobulin
 CC capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL-
 CC -2 receptor; treating T-cell mediated disorders in a human patient
 CC comprising administering to the patient a therapeutic dose of an Ig; and
 CC a composition comprising a pure humanised Ig reactive with the p75 chain
 CC of the human IL-2 receptor. The method is used for designing a humanised
 CC immunoglobulin chain, useful for treating T-cell mediated disorders in a
 CC human patient. The invented method produces an Ig chain that is easily
 CC and economically produced. This is the amino acid sequence of mouse CMV5
 CC antibody light chain variable region. Residues from the human antibody
 CC framework can be replaced with residues from the mouse antibody to create
 CC a humanised antibody.

XX Sequence 107 AA;

XX Query Match

XX Best Local Similarity 80.3%; Score 531; DB 8; Length 107;

XX Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

XX 21 DIVLTGSPATLTSTPGDVSLSGRASQIISNNLHWYQKSHSPRLIKYASQISIGIPS 80

XX 1 DIVLTGSPATLTSTPGDVSLSGRASQIISNNLHWYQKSHSPRLIKYASQISIGIPS 60

XX Db

XX

XX

XX

XX

XX

QY 81 RFGSGSGTDFTLTINSVETEDFGMFCQGSNSWPLTFSGTLEIK 127
 Db 61 RFGSGSGTDFTLTINSVETEDFGMFCQGSNSWPLTFSGTLEIK 107

RESULT 14

ID ADE85713 standard; protein; 107 AA.

XX ADE85713;

DT 12-FEB-2004 (first entry)

XX Human EphA2 antibody Eph098B-233.152 VL chain protein SEQ ID NO:17.

XX cancer; hyperproliferative cell disease; EphA2 antibody;

XX EphA2 agonistic antibody; cytostatic; antiasthmatic; antipsoriatic;

XX antiinflammatory; vasotropic; respiratory; gene therapy;

XX metastatic cancer; asthma; psoriasis; inflammatory bowel disease;

XX smooth muscle restenosis; endothelial restenosis; Crohn's disease;

XX chronic obstructive pulmonary disease; human.

XX Homo sapiens.

XX WO2003094859-A2.

XX 20-NOV-2003.

XX 12-MAY-2003; 2003WO-US015044.

XX 10-MAY-2002; 2002US-0379322P.

XX 14-OCT-2002; 2002US-0418213P.

XX 03-APR-2003; 2003US-0460507P.

XX (MED1-) MEDIMUNE INC.

XX Kinch MS, Carles-Kinch K, Kiener P, Langermann S;

XX WPI; 2004-012002/01.

XX N-PSDB; ADE85721.

XX Treating cancer or a non-cancer hyperproliferative cell disease (e.g.
 PT asthma, psoriasis, inflammatory bowel disease or restenosis) in a patient
 PT comprises administering to the patient a therapeutic amount of an EphA2
 PT antibody.

XX Claim 52; SEQ ID NO 17; 173pp; English.

XX The present invention describes a method for treating cancer or a non-
 CC cancer hyperproliferative cell disease or disorder in a patient, which
 CC comprises administering to the patient a therapeutic amount of an EphA2
 CC antibody (1) that is an EphA2 agonistic antibody, an EphA2 cancer cell
 CC phenotype inhibiting antibody, an exposed EphA2 epitope antibody, or an
 CC antibody that binds EphA2 with a K-off of less than 3 x 10⁻³ s⁻¹. Also
 CC described: (1) a pharmaceutical composition comprising a therapeutic
 CC amount of (1) and a pharmaceutical carrier; (2) a cell line that produces
 CC (1); (3) a hybridoma deposited with the ATCC accession number PTA-4572,
 CC PTA-4573 or PTA-4574; (4) an isolated nucleic acid comprising a
 CC nucleotide sequence encoding a light chain variable domain or a heavy
 CC chain variable domain of the EphA2 antibody; (5) a vector comprising the
 CC nucleic acid described above; (6) a host cell comprising the vector; (7)
 CC methods of identifying the EphA2 agonistic antibody or the EphA2 antibody
 CC that inhibits a cancer cell phenotype, that kills cancer cells having a
 CC cancer cell phenotype or that preferentially binds an EphA2 epitope
 CC exposed on cancer cells; and (8) a method of diagnosing, prognosing or
 CC monitoring the efficacy of therapy for cancer in a patient known to or
 CC suspected to have cancer. (1) has cytostatic, antiasthmatic,
 CC antipsoriatic, antiinflammatory, vasotropic and respiratory activities,
 CC and can be used in gene therapy. The composition and methods are useful
 CC in managing, diagnosing, preventing or treating hyperproliferative cell
 CC diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell
 CC diseases or disorders, such as asthma, psoriasis, inflammatory bowel
 CC disease, smooth muscle restenosis, endothelial restenosis, Crohn's

CC disease or chronic obstructive pulmonary disease. They may also be used
CC for monitoring the efficacy of therapy for cancer in a patient known to
CC or suspected to have cancer, and in screening for anti-cancer drugs. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 107 AA;

Query Match 80.0%; Score 529; DB 8; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.7e-30;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYASQSIGIPS 80
DB 1 DIVLTQSPATLSVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYVFGSIGIPS 60
QY 81 RPSGSGSGTDFLTLSINSVETEDFGMYFCQOQNSMWPPLTFSGTKLEIK 127
DB 61 RPSGSGSGTDFLTLSINSVETEDFGMYFCQOQNSMWPPLTFGAGTKLEIK 107

RESULT 15

ID AAR38601 standard; peptide; 107 AA.

XX AAR38601;

XX 25-MAR-2003 (revised)

DT 28-OCT-1993 (first entry)

XX HYH light chain.

XX Antibody; variable domain; light; L; heavy; H; consensus; affinity;
XX antigen; immunogenicity; humanisation; framework.

OS Homo sapiens.

PN MO9311794-A1.

XX 24-JUN-1993.

XX 14-DEC-1992; 92WO-US010906.

XX 13-DEC-1991; 91US-00808464.

XX (XOMA) XOMA CORP.

XX Studnicka GM, Little RG, Fishwild DM, Kohn FR;

DR WPI; 1993-213827/26.

XX Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but retain
PT binding affinity, etc.

PS Disclosure; Page 84; 160pp; English.

XX The amino acid sequences of the light and heavy chains of the variable
CC domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex] (AAR38601 and
CC AAR38608, respectively), MCPC [IGA Fab MCPC603-phosphocholine complex]
CC (AAR38602-03 and AAR38609-10, respectively), NEMW [IG Fab' NEM] (AAR38604
CC -05 and AAR38611, respectively) and KOL [IGG1 KOL] (AAR38606-07 and
CC AAR38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made. Unlike other methods of humanisation,
CC which advocate the replacement of entire antibody framework regions with
CC those of human antibodies, this method involves only the introduction of
CC human residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody are not
CC diminished. (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 107 AA;

Query Match 79.6%; Score 526; DB 2; Length 107;
Best Local Similarity 94.4%; Pred. No. 2.7e-30;

Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYASQSIGIPS 80
DB 1 DIVLTQSPATLSVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYVFGSIGIPS 60
QY 81 RPSGSGSGTDFLTLSINSVETEDFGMYFCQOQNSMWPPLTFSGTKLEIK 127
DB 61 RPSGSGSGTDFLTLSINSVETEDFGMYFCQOQNSMWPPLTFGAGTKLEIK 107

Search completed: May 25, 2005, 15:47:16
Job time : 63.2493 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 15.9553 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661
Sequence: 1 MVEFPOILGLMFMISASRG.....QOSNSWPLTFGSGTKLEIKR 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	96.4	127	1	US-08-436-463-18 Sequence 18, Appl
2	634	95.9	127	1	US-07-634-278-83 Sequence 83, Appl
3	634	95.9	127	1	US-08-477-728-83 Sequence 83, Appl
4	634	95.9	127	1	US-08-474-040-83 Sequence 83, Appl
5	634	95.9	127	1	US-08-487-200-83 Sequence 83, Appl
6	634	95.9	127	3	US-08-484-537-83 Sequence 4, Appl
7	622	94.1	127	1	US-08-436-463-4 Sequence 4, Appl
8	534	80.8	108	4	US-09-332-290-27 Sequence 27, Appl
9	534	80.8	109	1	US-07-942-245-4 Sequence 4, Appl
10	531	80.3	107	1	US-07-634-278-62 Sequence 62, Appl
11	531	80.3	107	1	US-08-477-728-62 Sequence 62, Appl
12	531	80.3	107	1	US-08-474-040-62 Sequence 62, Appl
13	531	80.3	107	1	US-08-487-200-62 Sequence 62, Appl
14	531	80.3	107	3	US-08-484-537-62 Sequence 62, Appl
15	529	80.0	107	1	US-08-436-463-20 Sequence 20, Appl
16	526	79.6	107	1	US-08-107-659D-1 Sequence 1, Appl
17	526	79.6	107	1	US-08-472-788A-1 Sequence 1, Appl
18	526	79.6	107	2	US-08-477-531B-1 Sequence 1, Appl
19	526	79.6	107	2	US-08-485-246A-1 Sequence 1, Appl
20	511	77.3	107	4	US-08-082-842A-1 Sequence 8, Appl
21	511	77.3	107	4	US-09-339-922A-8 Sequence 8, Appl
22	511	77.3	107	4	US-08-791-391A-8 Sequence 8, Appl
23	511	77.3	107	4	US-09-016-061-8 Sequence 8, Appl
24	506	76.6	100	1	US-08-436-463-19 Sequence 19, Appl
25	492	74.4	259	4	US-09-419-788-29 Sequence 29, Appl
26	480	72.6	103	4	US-08-436-463-21 Sequence 21, Appl
27	471	71.3	108	3	US-09-247-352-1 Sequence 1, Appl
27	471	71.3	108	4	US-09-466-635-1 Sequence 1, Appl

28	471	71.3	214	3	US-09-247-352-4 Sequence 4, Appl
29	471	71.3	214	4	US-09-466-635-4 Sequence 4, Appl
30	468.5	70.9	127	2	US-08-476-176B-6 Sequence 6, Appl
31	468.5	70.9	127	3	US-08-127-721A-6 Sequence 6, Appl
32	468.5	70.9	127	3	US-08-485-246A-6 Sequence 6, Appl
33	468.5	70.9	127	2	US-08-737-560A-11 Sequence 11, Appl
34	467.5	70.7	127	2	US-08-476-176B-10 Sequence 10, Appl
35	467.5	70.7	127	3	US-08-127-721A-10 Sequence 10, Appl
36	467.5	70.7	127	2	US-08-485-246A-10 Sequence 10, Appl
37	467.5	70.7	127	2	US-08-653-402B-8 Sequence 8, Appl
38	464.5	70.3	127	2	US-08-476-176B-8 Sequence 8, Appl
39	464.5	70.3	127	3	US-08-127-721A-8 Sequence 8, Appl
40	464.5	70.3	127	3	US-08-485-246A-8 Sequence 8, Appl
41	455	68.8	107	4	US-09-438-954-38 Sequence 38, Appl
42	442	66.9	107	1	US-07-634-278-63 Sequence 63, Appl
43	442	66.9	107	1	US-07-634-278-87 Sequence 87, Appl
44	442	66.9	107	1	US-08-477-728-63 Sequence 63, Appl
45	442	66.9	107	1	US-08-477-728-87 Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-08-436-463-18
Sequence 18, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoko
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-PELVINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: KIMACHI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-463-18
Query Match 96.4%; Score 637; DB 1; Length 127;
Best Local Similarity 96.9%; Pred. No. 2.7e-53;
Matches 123; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 61 HESPRLIKYASQSIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCQOQSNMPLTFGS 120
 QY 121 GTRLEIK 127
 Db 121 GTRLEIK 127

RESULT 4

US-08-474-040-83
 ; Sequence 83, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold B.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,040
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 83:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-474-040-83

Query Match 95.9%; Score 634; DB 1; Length 127;
 Best Local Similarity 96.1%; Pred. No. 5, 2e-53;
 Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WFTPTQIIIGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
 DB 1 WFTPTQIIIGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
 QY 61 HESPRLIKYASQSIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCQOQSNMPLTFGS 120

Db 61 HESPRLIKYASQSIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCQOQSNMPLTFGS 120
 QY 121 GTRLEIK 127
 Db 121 GTRLEIK 127

RESULT 5

US-08-487-200-83
 ; Sequence 83, Application US/08487200
 ; Patent No. 5693762
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold B.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,200
 ; FILING DATE: 7-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002610
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 83:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-487-200-83

Query Match 95.9%; Score 634; DB 1; Length 127;
 Best Local Similarity 96.1%; Pred. No. 5, 2e-53;
 Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WFTPTQIIIGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
 DB 1 WFTPTQIIIGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
 QY 61 HESPRLIKYASQSIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCQOQSNMPLTFGS 120

Db 61 HESPRLLIKYASOSISGIPSRFSGSGGTDFTLSVNGVETEDFGMYFCQGSNSWPHTFGG 120
Qy 121 GTKLEIK 127
Db 121 GTKLEIK 127

RESULT 6
US-08-484-537-83
; Sequence 83, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US/07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-537-83

Query Match 95.9%; Score 634; DB 3; Length 127;
Best Local Similarity 96.1%; Pred. No. 5,2e-53;
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
Db 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
Qy 61 HESPRLLIKYASOSISGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120
Db 61 HESPRLLIKYASOSISGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPHTFGG 120

Qy 121 GTKLEIK 127
Db 121 GTKLEIK 127

RESULT 7
US-08-436-463-4
; Sequence 4, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoko
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-4

Query Match 94.1%; Score 622; DB 1; Length 127;
Best Local Similarity 94.5%; Pred. No. 7,2e-52;
Matches 120; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
Db 1 MVSSPOLGLMLFWISASRGDIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60
Qy 61 HESPRLLIKYASOSISGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120
Db 61 HESPRLLIKYASOSISGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQGSNSWPHTFGA 120
Qy 121 GTKLEIK 127
Db 121 GTKLEIK 127
RESULT 8
US-09-232-290-27
; Sequence 27, Application US/09232290A
; Patent No. 6815540

GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 27
LENGTH: 108
TYPE: PRT
ORGANISM: Murine
US-09-232-290-27

Query Match 80.8%; Score 534; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 1.4e-43;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSGCRASQIISNNLHWYQOKSHSPRLLIKYSQSIGIPS 80
DB 1 DIVLTQSPATLSVTPGNSVSVLSGCRASQISGNNLHWYQOKSHSPRLLIKYSQSIGIPS 60
QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTFGGTKLEIKR 128
DB 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTFGGTKLEIKR 108

RESULT 9

US-07-942-245-4
Sequence 4, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-4

Query Match 80.8%; Score 534; DB 1; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.4e-43;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSGCRASQIISNNLHWYQOKSHSPRLLIKYSQSIGIPS 80
DB 1 DIVLTQSPATLSVTPGNSVSVLSGCRASQISGNNLHWYQOKSHSPRLLIKYSQSIGIPS 60
QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTFGGTKLEIKR 128
DB 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTFGGTKLEIKR 108

RESULT 10

US-07-634-278-62
Sequence 62, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHREIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: SELICK, Kathleen L.
APPLICANT: COELING, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-62

Query Match 80.3%; Score 531; DB 1; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSGCRASQIISNNLHWYQOKSHSPRLLIKYSQSIGIPS 80
DB 1 DIVLTQSPATLSVTPGNSVSVLSGCRASQISGNNLHWYQOKSHSPRLLIKYSQSIGIPS 60

Db 1 DIVLTGSPATLSTVPDGSVLSLSCRASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 60
QY 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPHTFGGGTLEIK 107

RESULT 11
US-08-477-728-62
; Sequence 62, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-728-62

Query Match 80.3%; Score 531; DB 1; Length 107;
Best Local Similarity 95.3%; Pred. No. 2,6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 21 DIVLTGSPATLSTVPDGSVLSLSCRASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 80
Db 1 DIVLTGSPATLSTVPDGSVLSLSCRASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 60
QY 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPHTFGGGTLEIK 107

RESULT 12
US-08-474-040-62
; Sequence 62, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Knourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-62

Query Match 80.3%; Score 531; DB 1; Length 107;
Best Local Similarity 95.3%; Pred. No. 2,6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 21 DIVLTGSPATLSTVPDGSVLSLSCRASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 80
Db 1 DIVLTGSPATLSTVPDGSVLSLSCRASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 60
QY 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNSWPHTFGGGTLEIK 107
RESULT 13
US-08-487-200-62
; Sequence 62, Application US/08487200

```
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLF, Nicholas P.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-62

Query Match      80.3%; Score 531; DB 1; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 80
DB 1 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 60

QY 81 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127
DB 61 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 14
US-08-484-537-62
; Sequence 62, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
```

```
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLF, Nicholas P.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-62

Query Match      80.3%; Score 531; DB 3; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 80
DB 1 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 60

QY 81 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127
DB 61 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 15
US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroyaki
; APPLICANT: NISHIYAMA, Kiyocho
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-BELINE HERPES VIRUS-1 RECOMBINANT
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 59.0586 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

Sequence: 1 MWFTQIIIGLMLFWISASRG.....QQSNMPLTFSGTLEIKR 128

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	661	100.0	128	13	US-10-006-773-6 Sequence 6, Appl1
2	634	95.9	127	15	US-10-452-357-83 Sequence 83, Appl1
3	626	94.7	127	15	US-10-389-155-70 Sequence 70, Appl1
4	626	94.7	127	15	US-10-452-646-28 Sequence 28, Appl1
5	614	92.9	127	15	US-10-308-817-123 Sequence 123, Appl1
6	533	80.6	107	15	US-10-453-698-123 Sequence 123, Appl1
7	533	80.6	107	15	US-10-389-155-21 Sequence 21, Appl1
8	531	80.3	107	15	US-10-389-417-21 Sequence 21, Appl1
9	531	80.3	107	15	US-10-452-357-62 Sequence 62, Appl1
10	531	80.3	107	15	US-10-436-782-17 Sequence 17, Appl1
11	529	80.0	107	17	US-10-923-068-511 Sequence 511, Appl1
12	529	80.0	107	17	US-10-920-899-1776 Sequence 1776, Appl1

14	526	79.6	107	15	US-10-340-189-1	Sequence 1, Appl1
15	526	79.6	107	15	US-10-325-696-1	Sequence 1, Appl1
16	525	79.6	109	14	US-10-078-757B-45	Sequence 45, Appl1
17	520	78.7	108	10	US-09-910-483-38	Sequence 38, Appl1
18	520	78.7	108	10	US-09-910-483-42	Sequence 42, Appl1
19	518	78.4	108	14	US-10-223-880-7	Sequence 7, Appl1
20	511	77.3	107	8	US-08-790-540A-8	Sequence 8, Appl1
21	511	77.3	107	8	US-08-791-391A-8	Sequence 8, Appl1
22	511	77.3	107	10	US-09-900-500-8	Sequence 8, Appl1
23	511	77.3	107	14	US-10-305-231-8	Sequence 8, Appl1
24	511	77.3	107	15	US-10-452-440-8	Sequence 8, Appl1
25	511	77.3	107	15	US-10-463-847-8	Sequence 8, Appl1
26	511	77.3	107	17	US-10-959-871-8	Sequence 8, Appl1
27	506	76.6	127	15	US-10-374-600-15	Sequence 15, Appl1
28	506	76.6	127	15	US-10-374-531-15	Sequence 15, Appl1
29	493	74.6	127	15	US-10-374-600-5	Sequence 5, Appl1
30	493	74.6	127	15	US-10-374-531-5	Sequence 5, Appl1
31	493	74.6	127	15	US-10-374-600-11	Sequence 11, Appl1
32	493	74.6	127	15	US-10-374-531-11	Sequence 11, Appl1
33	492.5	74.5	109	13	US-10-032-482-6	Sequence 6, Appl1
34	492	74.4	264	14	US-10-207-655-400	Sequence 400, Appl1
35	492	74.4	548	14	US-10-207-655-272	Sequence 272, Appl1
36	487	73.7	127	14	US-10-207-655-264	Sequence 264, Appl1
37	484.5	73.3	131	14	US-10-207-655-244	Sequence 244, Appl1
38	484.5	73.3	267	14	US-10-207-655-248	Sequence 248, Appl1
39	484.5	73.3	552	14	US-10-207-655-265	Sequence 265, Appl1
40	471	71.3	768	14	US-10-207-655-350	Sequence 350, Appl1
41	467	70.7	243	14	US-10-097-558-2	Sequence 2, Appl1
42	466	70.5	107	10	US-09-982-464-1	Sequence 1, Appl1
43	466	70.5	107	16	US-10-697-399-1	Sequence 1, Appl1
44	466	70.5	107	17	US-10-697-400-1	Sequence 1, Appl1
45	465	70.3	128	15	US-10-443-466A-74	Sequence 74, Appl1

ALIGNMENTS

RESULT 1
US-10-006-773-6
; Sequence 6, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant.
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-6

Query Match 100.0%; Score 661; DB 13; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWFTQIIIGLMLFWISASRGDIVLTPSPATISVTGDSVSLSCRAQSQTISNNLHWYQKS 60
DB 1 MWFTQIIIGLMLFWISASRGDIVLTPSPATISVTGDSVSLSCRAQSQTISNNLHWYQKS 60
QY 61 HSPPLIKRYASQSTSGIPSRFSGSGSGDFLTSINVTETDFPGMYFCQSNMPLTFGS 120
DB 61 HSPPLIKRYASQSTSGIPSRFSGSGSGDFLTSINVTETDFPGMYFCQSNMPLTFGS 120
QY 121 GTKLEIKR 128
DB 121 GTKLEIKR 128

RESULT 2
US-10-452-357-83
; Sequence 83, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William
; APPLICANT: Landolfi, Nicholas
; APPLICANT: Coeltingh, Kathleen
; APPLICANT: Selick, Harold
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; FILE REFERENCE: 05882.0078, CNU501
; CURRENT APPLICATION NUMBER: US/10/452,357
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/718,993
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/487,200
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/634,278
; PRIOR FILING DATE: 1990-12-19
; PRIOR APPLICATION NUMBER: 07/590,275
; PRIOR FILING DATE: 1990-09-28
; PRIOR APPLICATION NUMBER: 07/310,252
; PRIOR FILING DATE: 1989-02-13
; PRIOR APPLICATION NUMBER: 07/290,975
; PRIOR FILING DATE: 1988-12-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CMV5 light chain antibody
US-10-452-357-83

Query Match 95.9%; Score 634; DB 15; Length 127;
Best Local Similarity 96.1%; Pred. No. 6,5e-48;
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MVTPTQILGLMFWISASRGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKS 60
DB 1 MVTPTQILGLMFWISASRGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKS 60
QY 61 HESPRLLIKYASQISIGIPSRFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPPTFGS 120
DB 61 HESPRLLIKYASQISIGIPSRFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPPTFGS 120
QY 121 GTKLEIK 127
DB 121 GTKLEIK 127

RESULT 3
US-10-389-155-70
; Sequence 70, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coeltingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-389-155-70

Query Match 94.7%; Score 626; DB 15; Length 127;
Best Local Similarity 94.5%; Pred. No. 3.3e-47;
Matches 120; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 MVTPTQILGLMFWISASRGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKS 60
DB 1 MVTPTQILGLMFWISASRGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKS 60
QY 61 HESPRLLIKYASQISIGIPSRFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPPTFGS 120
DB 61 HESPRLLIKYASQISIGIPSRFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPPTFGS 120
QY 121 GTKLEIK 127
DB 121 GTKLEIK 127

RESULT 4
US-10-389-417-70
; Sequence 70, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William P.
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Coeltingh, Kathleen L.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

```
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/389,417
/ FILING DATE: 13-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/325,000
/ FILING DATE: 01-JUN-1999
/ APPLICATION NUMBER: US 07/290,975
/ FILING DATE: 28-DEC-1988
/ APPLICATION NUMBER: US 07/310,252
/ FILING DATE: 13-FEB-1989
/ APPLICATION NUMBER: US 07/590,274
/ FILING DATE: 28-SEP-1990
/ APPLICATION NUMBER: US 07/634,278
/ FILING DATE: 19-DEC-1990
/ APPLICATION NUMBER: US 08/484,537
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 011823-002650US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 127 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-389-417-70

Query Match          94.7%; Score 626; DB 15; Length 127;
Best Local Similarity 94.5%; Pred. No. 3.3e-47;
Matches 120; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MWFTPOLGLMLFWISASRGDIIVLTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKS 60
    |||||
DB 1 MWFTPOLGLMLFWISASRGDIIVLTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKS 60

QY 61 HSPRLIRYASQISIGIPSRFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFG 120
    |||||
DB 61 HSPRLIRYASQISIGIPSRFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFG 120

QY 121 GTKLEIK 127
    |||||
DB 121 GTKLEIK 127

RESULT 5
US-10-452-646-28
/ Sequence 28, Application US/10452646
/ Publication No. US20040018593A1
/ GENERAL INFORMATION:
/ APPLICANT: Carton, Jill M.
/ APPLICANT: Staquet, Kimberly C.
/ APPLICANT: Scallion, Bernard J.
/ APPLICANT: Jili, Gilles-Komar
/ TITLE OF INVENTION: ANTI-REL FUSION ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CHN296 NP
/ CURRENT APPLICATION NUMBER: US/10/452,646
/ PRIOR APPLICATION NUMBER: 2003-06-02
/ PRIOR FILING DATE: 2002-06-03
```

```
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 28
/ LENGTH: 127
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-452-646-28

Query Match          92.9%; Score 614; DB 15; Length 127;
Best Local Similarity 91.3%; Pred. No. 3.7e-46;
Matches 116; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 MWFTPOLGLMLFWISASRGDIIVLTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKS 60
    |||||
DB 1 MWFTPOLGLMLFWISASRGDIIVLTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKS 60

QY 61 HSPRLIRYASQISIGIPSRFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFG 120
    |||||
DB 61 HSPRLIRYASQISIGIPSRFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFG 120

QY 121 GTKLEIK 127
    |||||
DB 121 GTKLEIK 127

RESULT 6
US-10-308-817-123
/ Sequence 123, Application US/10308817
/ Publication No. US20030219861A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Dayang
/ APPLICANT: Rocher, Russell
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 123
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: mouse
US-10-308-817-123

Query Match          80.6%; Score 533; DB 15; Length 107;
Best Local Similarity 96.3%; Pred. No. 3.7e-39;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIP 80
    |||||
DB 1 DIVTQSPATLSVTPGDVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIP 80

QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127
    |||||
DB 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 107

RESULT 7
US-10-453-698-123
/ Sequence 123, Application US/10453698
/ Publication No. US20040038308A1
/ GENERAL INFORMATION:
/ APPLICANT: Rocher, Russell
/ APPLICANT: Roche, Russell
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 82 CIP (1087-37 CIP)
/ CURRENT APPLICATION NUMBER: US/10/453,698
/ CURRENT FILING DATE: 2003-06-03
/ NUMBER OF SEQ ID NOS: 196
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 123
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: mouse
```

US-10-453-698-123

Query Match	80.6%	Score 533;	DB 15;	Length 107;
Best Local Similarity	96.3%;	Pred. No. 3.7e-39;		
Matches 103; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	Dy
21	1
DIYVTOGPATLSVTPGDSVSLSCASQSI	DIYVTOGPATLSVTPGDSVSLSCASQSI
INNNLHWQOKHESPRLILKAQSAISIGIS	INNNLHWQOKHESPRLILKAQSAISIGIS
8	6
81	81
RFSSGSGCTPETSINSVEETEDFCMYCOOSNMPILRFSGCTLEIK	RFSSGSGCTPETSINSVEETEDFCMYCOOSNMPILRFSGCTLEIK
127	127
61	61
RFSSGSGGIDPILSINSVEETEDFCMYCOOSNMPITFGGGLKLEIK	RFSSGSGGIDPILSINSVEETEDFCMYCOOSNMPITFGGGLKLEIK
107	107

RESULT 8
US-10-389-155-21

Sequence 21, Application US/103891555
Publication No. US20030229208A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.

APPLICANT: Queen, Cary L.
Co, Man Sung
Schneider, William P.
Landolfi, Nicholas P.
Coelrich, Kathleen L.
Selick, Harold B.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
ATTORNEY: (415) 555-0000

FORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION:	SEQ ID NO:
US-10-389-155-21	21:

Query Match	80.3%;	Score 531;	DB 15;	Length 107;
Best Local Similarity	95.3%;	Pred. No. 5.5e-39;		
Matches 102;	Conservative 1;	Mismatches 4;	Indels	

QY	Db	QY	Db
2	1	81	61
DIYLTSPPTLSTVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIRIYASQSIGIS	DIYLTSPPTLSTVTPEDSVSLSCRAQIISNNLHWYQOKSHSPRLIRIYASQSIGIS	REGSSSGDFTLISVETPEPGMFFCOOSNSWPLTFSSGKLEIK	REGSSSGDFTLISVNGETEDPGMFFCOOSNSWPLTFSSGKLEIK
80	60	127	107

RESULT 9
US-10-389-417-21

; Sequence 21, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:

APPLICANT: Queen, Cary L.
Co, Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelingh, Kathleen L.

COMPUTER READABLE FORM:

```

?
? MEDIUM TYPE: floppy disk
?
? COMPUTER: IBM PC compatible
?
? OPERATING SYSTEM: PC-DOS/MS-DOS
?
? SOFTWARE: Patentin Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA: 06/03/0000 0000
?

```

APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/325,000
 ? FILING DATE: 01-JUN-1999
 ? APPLICATION NUMBER: US 07/290,973
 ? FILING DATE: 28-DEC-1988
 ? APPLICATION NUMBER: US 07/310,252
 ? FILING DATE: 13-FEB-1989
 ? APPLICATION NUMBER: US 07/590,274
 ? FILING DATE: 28-SEP-1990
 ? APPLICATION NUMBER: US 07/634,278
 ? FILING DATE: 19-DEC-1990
 ? APPLICATION NUMBER: US 08/484,537
 ? FILING DATE: 07-JUN-1995

NAME: Smith, William N

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
FAX: (415) 576-0200

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids

```

;      TYPE: amino acid
;      STRANDEDNESS: <Unknown>
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein

```

SEQUENCE	DESCRIPTION:	SEQ ID NO:	21
US-10-389-417-21			

Query Match 80.3%; Score 531; DB 15; Length 107;

Best Local Similarity 95.3%; Pred. No. 5.5e-39;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 80
Db 1 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

RESULT 10
US-10-452-357-62
Sequence 62, Application US/10452357
Publication No. US20040058414A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary

APPLICANT: Co, Man Sung

APPLICANT: Schneider, William

APPLICANT: Landolfi, Nicholas

APPLICANT: Coeligh, Kathleen

APPLICANT: Selick, Harold

TITLE OF INVENTION: Improved Humanized Immunoglobulins

FILE REFERENCE: 05882.0078, CUS01

CURRENT APPLICATION NUMBER: US/10/452,357

PRIOR FILING DATE: 2003-05-30

PRIOR APPLICATION NUMBER: 09/718,993

PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 09/487,200

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 07/634,278

PRIOR FILING DATE: 1990-12-19

PRIOR APPLICATION NUMBER: 07/590,275

PRIOR FILING DATE: 1990-09-28

PRIOR APPLICATION NUMBER: 07/310,252

PRIOR FILING DATE: 1989-02-13

PRIOR APPLICATION NUMBER: 07/290,975

PRIOR FILING DATE: 1988-12-28

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.2

SEQ ID NO 62

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: murine Cmu5 light chain antibody

US-10-452-357-62

Query Match 80.3%; Score 531; DB 15; Length 107;
Best Local Similarity 95.3%; Pred. No. 5.5e-39;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 80
Db 1 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

RESULT 11
US-10-436-782-17
Sequence 17, Application US/10436782
Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kiener, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097

CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322

PRIOR FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/418,213

PRIOR FILING DATE: 2002-10-14

PRIOR APPLICATION NUMBER: 60/418,213

PRIOR FILING DATE: 2003-04-03

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn version 3.2

SEQ ID NO 17

LENGTH: 107

TYPE: PRT

ORGANISM: Homo sapiens

US-10-436-782-17

Query Match 80.0%; Score 529; DB 15; Length 107;
Best Local Similarity 94.4%; Pred. No. 8.3e-39;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 80
Db 1 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

RESULT 12
US-10-923-068-511
Sequence 511, Application US/10923068
Publication No. US20050042664A1

GENERAL INFORMATION:

APPLICANT: Wu, Herren

APPLICANT: Dall'Acqua, William

APPLICANT: Damachroder, Melissa

TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES

FILE REFERENCE: AB600US

CURRENT APPLICATION NUMBER: US/10/923,068

NUMBER OF SEQ ID NOS: 518

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 511

LENGTH: 107

TYPE: PRT

ORGANISM: Mus musculus

US-10-923-068-511

Query Match 80.0%; Score 529; DB 17; Length 107;
Best Local Similarity 94.4%; Pred. No. 8.3e-39;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 80
Db 1 DIVTQSPATLSTVTPGDSVSLSCRASQISNNLHMWYQKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127
Db 61 RFGSGSGTDFTLTSLNSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

RESULT 13
US-10-920-899-1776
Sequence 1776, Application US/10920899
Publication No. US20050048617A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damachroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AB600US
CURRENT APPLICATION NUMBER: US/10/920,899

CURRENT FILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 1781
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1776
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-10-920-899-1776

Query Match 80.0%; Score 529; DB 17; Length 107;
Best Local Similarity 94.4%; Pred. No. 8,3e-39;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHESPRLIKYASQSIGIPS 80
1 DIVLTOSPATLSTVPDGSVSLSCRAQSIISNNLHMWYQOKSHESPRLIKYVFOISIGIPS 60

QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGSGTLEIK 127
Db 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGAGTLEIK 107

RESULT 14

US-10-340-189-1
Sequence 1, Application US/10340189
Publication No. US20030229207A1

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-340-189-1

Query Match 79.6%; Score 526; DB 15; Length 107;

Best Local Similarity 94.4%; Pred. No. 1.5e-38;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHESPRLIKYASQSIGIPS 80
Db 1 DIVLTOSPATLSTVPDGSVSLSCRAQSIISNNLHMWYQOKSHESPRLIKYASQSIGIPS 60

QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGSGTLEIK 127
Db 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGAGTLEIK 107

RESULT 15

US-10-325-696-1
Sequence 1, Application US/10325696
Publication No. US20040005630A1

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-325-696-1

Query Match 79.6%; Score 526; DB 15; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.5e-38;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHESPRLIKYASQSIGIPS 80
Db 1 DIVLTOSPATLSTVPDGSVSLSCRAQSIISNNLHMWYQOKSHESPRLIKYASQSIGIPS 60

QY 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGSGTLEIK 127
Db 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOSNSWPLTFGAGTLEIK 107

Thu May 26 09:14:28 2005

us-10-006-773a-6.rapb

Page 7

Search completed: May 25, 2005, 16:06:50
Job time : 60.1836 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 / Search time 18.0986 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

Sequence: 1 MVFTPOILGLMLFMSASRG.....QQNSNWPITFGSGTKLEIKR 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	97.1	138	2	A26471
2	592	89.6	123	2	S35479
3	531	80.3	107	2	A45722
4	530	80.2	107	2	B45722
5	524	79.3	104	2	B43413
6	524	79.3	106	2	PL0267
7	507	76.7	102	2	S26346
8	506	76.6	107	2	C45722
9	473	71.6	128	2	PN0445
10	465	70.3	115	1	KVMSL7
11	447	67.6	108	2	C30502
12	425	64.3	103	2	S19975
13	423	64.0	144	2	PL0106
14	422	63.8	128	2	S40343
15	420	63.5	128	2	S40379
16	417.5	63.2	128	1	K3HU41
17	416	62.9	117	2	S40362
18	415	62.9	128	2	A56701
19	409	61.9	96	2	G33730
20	404	61.1	129	2	A33274
21	399	60.4	115	2	S10146
22	398	60.2	114	2	S00996
23	398	60.2	125	2	S40316
24	398	60.2	127	2	S40367
25	398	60.2	128	2	S40345
26	397	60.1	125	2	S40349
27	395	59.8	123	2	S40331
28	395	59.8	234	2	S01320
29	394	59.6	125	2	S40344

30	394	59.6	127	2	S04574	Ig kappa chain pre
31	391.5	59.2	131	2	S40328	Ig kappa chain - h
32	391	59.2	122	2	S40314	Ig kappa chain - h
33	391	59.2	129	2	S49532	anti-5m antibody V
34	391	59.2	132	2	S40334	Ig kappa chain h
35	390	59.0	125	2	S40333	Ig kappa chain V-J
36	389	58.9	129	2	S29627	Ig kappa chain V r
37	389	58.9	130	2	S40360	Ig kappa chain - h
38	388	58.7	108	2	S19674	Ig kappa chain V r
39	388	58.7	129	1	K3HU4A	Ig kappa chain pre
40	388	58.7	145	2	PL0014	Ig kappa chain pre
41	386	58.4	111	2	S23628	Ig kappa chain V r
42	386	58.4	129	2	S40369	Ig kappa chain - h
43	385	58.2	129	1	K3HUH1	Ig kappa chain pre
44	384.5	58.2	136	2	S40357	Ig kappa chain V-J
45	384.5	58.2	215	2	JEB0244	Ig kappa chain NIG

ALIGNMENTS

RESULT 1

A26471

Ig kappa chain precursor V region (MAX33) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C:Accession: A26471

R:Buckel, P.; Hubner-Parajsz, C.; Matthes, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine

A:Reference number: A91572; PMID:87248058; PMID:3110009

A:Accession: A26471

A:Molecule type: mRNA

A:Residues: 1-138 <BUC>

A:Cross-references: GB:M6162; NID:g196893; PIDN:AAA38823.1; PID:g196894

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 97.1%; Score 642; DB 2; Length 138;

Best Local Similarity 96.9%; Pred. No. 1.7e-47;

Matches 124; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVFTPOILGLMLFMSASRGDIVLTQSPATLSVTPGDSVSLSCRAQSIIISNNLHWYQOKS 60

DB 1 MVFTPOILGLMLFMSASRGDIVLTQSPATLSVTPGDSVSLSCRAQSIIISNNLHWYQOKS 60

QY 61 HESPRLLIKVASQSIISGIPSPFGSGSGNDFTLSINSVETEDFGMYPCQNSNWPITFGS 120

DB 61 HESPRLLIKVASQSIISGIPSPFGSGSGNDFTLSINSVETEDFGMYPCQNSNWPITFGS 120

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

QY 121 GTKLEIKR 128

DB 121 GTKLEIKR 128

```
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-12/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>
```

Query Match	89.6%	Score 592	DB 2	length 123
Best Local Similarity	95.8%	Pred. No.	2.5e-43	
Matches 115	Conservative	0	Mismatches 5	Indels 0
			Gaps	0

Dy 9 GLMLFVISASRGDIVLTQSPATLSVTPGGSVSLSCRASQTISNNLHWYQQKSHESRLLI 68
|||||
Db 1 GLMLFWISASRGDIVLTQSPATLSVTPGDKVSLSCRASQSISNYLHWYQQKSHESRPLLI 600
|||||

QY 69 KYASQISISGIPSRFSSGSGTDFTLINSVEDEDPGMYFCQOQNSWPLTFSGTKLEIKR 128
|||
Db 61 KYASQISISGIPSRFSSGSGTDFTLINSVEDEDPGMYFCQOQNSWPHTFSGTKLEIKR 120

RESULT 3
A45722

C:Accession: A45722
R:Stimpson, J.A.; Chow, J.C.; Baker, J.; Andaloivic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human immunodeficiency virus type 1 gp120
J:Reference number: A45722; MUID:93100833; PMID:7677958

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <STM>
A:Note: sequence extracted from NCBI backbone (NCBP_120589)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: glycoprotein
C:16-90/Domain: immunoglobulin homology <IMM>

```
Query Match:      80.3%   Score 531, DB 2, length 107,
Best Local Similarity 95.3%   Pred. No. 3, le=38,
Matches 102, Conservative 1, Mismatches 4, Indels 0, Gaps 0,
```

Oy 21 DIVLQSPATLSVTPGDSVSLSCRASQITSNLHMWYQQKSHESPELLIKTASQSISGIPS 80
D6 1 DIVLQSPATLSVTPGDSVSLSCRASQISNNLMHWYQQKSHESPELLIKTASQSISGIPS 60

```
QY      81  RFGSSSGTDTLINSVETEDFGMYFCQSSNSMPLTFGGTKLEIK 127
        |||||:|||||
Db      61  RFGSGSGTDTLINSVETEDFGMYFCQSSNSMPLTFGGTKLEIK 107
```

RESULT 4

A: anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (EPRC)
C: Species: Mus musculus (house mouse)
C: Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C: Accession: B45722
R: Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, A.
A: Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
P: Reference number: A45722; MUID:93100833; PMID:7677958

A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBI:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 C:16-90/Domain: immunoglobulin homology <IMM>

Query Match	80.2%;	Score 530;	DB 2;	Length 107;
Best Local Similarity	95.3%;	Pred. No. 3.8e-38;		

Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Dy 21 DIVLTQSPATLSTVPEDSVSLSCRASQGISNNLMHWQQKSHESRLLIKYASQSISGIPS 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIVLTQSPATLSTVPEDSVSLSCRASQGISNNLMHWQQKSHESRLLIKYASQSISGIPS 600

```

QY      81 RRSGGSGGTDFTLINSVETEDFGMYFCQQQSNMWPLTSGSGTKLEIK 127
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RRSGGSGGTDFTLINSVETEDFGMYFCQQQSNMWPHTFGGGKLEIK 107

```

RESULT 5
B43413
Tc kappa chain V region - mouse (fragment)

Cdate: 27-Apr1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
Caccession: B43413
R:Tomiyama, Y.; Brojster, E.; Ruggieri, Z.M.; Shattil, S.J.; Smiltnick, J.; Gorski, J.; Kun
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177; PMID:1517241

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <ROM>
A:Note: sequence extracted from NCBI backbone (NCBI:P_112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:13-87/Domain: immunoglobulin homology <Im>

Query Match	79.3%	Score 524	DB 2:	Length 104
Best Local Similarity	96.2%	Pred. No.	1 2e-37	
Matches 100, Conservative	3	Mismatches	1	Indels 0; Gaps 0;

Qy 24 LTQSPATLSTVTPGDSVSLSCASQIISNNLHWYQKSHSPRLLIKYSQSIGIPSRFS 83
Db 1 LTQSPATLSTVTPGDSVSLSCASQSIISNNLHWYQKSHSPRLLIKYSQSIGIPSRFS 60

```
QY      84 GSGGTDFTLSINSEVEDFGMYFCQQNSWPLTFGGSTRLEIK 127
        |||||
Db       61 GSGGTDFTLSINSEVEDFGMYFCQQNSWPLTFAGASKULEK 104
```

RESULT 6
PL0267
T. lucana sp. n. n. median (anti-DNA)
DN131721
mouse (4-6 months)

IG kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: P10267
R/Shomchik, M.; Masselli, M.; Shan, H.; Radic, M.Z.; Plesetsky, D.; Marshak-Rothstein, J.
R/Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: P10231, MUID:90111618, PMID:2104939

A;Accession: P10267
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match	79.3%	Score 524	DB 2	Length 106
Best Local Similarity	96.2%	Pred. NO.	1.2e-37	
Matches 102; Conservative	0	Mismatches	4	Indels 0; Gaps 0

21 DIVLTQSPATLSVTPGDSSVLSICRASQIIISNNLHWYQOKKHESPRLLIKYASQISGIPS 80

Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Dy 21 DIVLTQSPATLSTVPEDSVSLSCRASQGISNNLHMWQQKSHESRLLIKYASQSISGIPS 80
Db 1 DIVLTQSPATLSTVPEDSVSLSCRASQGISNNLMHWQQKSHESRLLIKYASQSISGIPS 600			

```

QY      81 RRSGGSGGTDFTLINSVETEDFGMYFCQQQSNMWPLTGGSGTKLEIK 127
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RRSGGSGGTDFTLINSVETEDFGMYFCQQQSNMWPHTFGGGKLEIK 107

```

RESULT 5
B43413
Tc kappa chain V region - mouse (fragment)

Cdate: 27-Apr1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
Caccession: B43413
R:Tomiyama, Y.; Brojster, E.; Ruggieri, Z.M.; Shattil, S.J.; Smiltnick, J.; Gorski, J.; Kun
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177; PMID:1517241

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <ROM>
A:Note: sequence extracted from NCBI backbone (NCBI:P_112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:13-87/Domain: immunoglobulin homology <Im>

Query Match	79.3%	Score 524	DB 2:	Length 104
Best Local Similarity	96.2%	Pred. No.	1 2e-37	
Matches 100, Conservative	3	Mismatches	1	Indels 0; Gaps 0;

Qy 24 LTQSPATLSTVTPGDSVSLSCASQIISNNLHWYQKSHSPRLLIKYSQSIGIPSRFS 83
Db 1 LTQSPATLSTVTPGDSVSLSCASQSIISNNLHWYQKSHSPRLLIKYSQSIGIPSRFS 60

```
QY      84 GSGGTDFTLSINSEVEDFGMYFCQQNSWPLTFGSGTKLEIK 127
        |||||
Db       61 GSGGTDFTLSINSEVEDFGMYFCQQNSWPLTFGAGSKULEK 104
```

RESULT 6
PL0267
T. lucana sp. n. n. median (anti-DNA)
DN131721
mouse (4-6 months)

IG kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C/Accession: P10267
R/Shomchik, M.; Masselli, M.; Shan, H.; Radic, M.Z.; Plesetsky, D.; Marshak-Rothstein, J.
R/Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: P10231, MUID:90111618, PMID:2104939

A;Accession: P10267
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match	79.3%	Score 524	DB 2	Length 106
Best Local Similarity	96.2%	Pred. NO.	1.2e-37	
Matches 102; Conservative	0	Mismatches	4	Indels 0; Gaps 0

21 DIVLTQSPATLSVTPGDSSVLSICRASQIIISNNLHWYQOKKHESPRLLIKYASQISGIPS 80

Db 1 DIVLTQSPATLSTVTPGDRVSLSCRAQSISNNLHWYQOKSHSPRLIKYASQISIGIPRS 60
QY 81 RFSSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 126
Db 61 RFSSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 106

RESULT 7
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 507; DB 2; Length 102;
Best Local Similarity 95.1%; Pred. No. 3.1e-36;
Matches 97; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 23 VLTPSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYASQISIGIPRS 82
Db 1 VLTPSPATLSTVTPGDSVSLSCRAQSISNNLHWYQOKSHSPRLIKYASQISIGIPRS 60
QY 83 SSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKL 124
Db 61 SSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKL 102

RESULT 8
C45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (H
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: C45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasequ
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: C45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120591)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 506; DB 2; Length 107;
Best Local Similarity 89.6%; Pred. No. 4e-36;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 22 IVLTSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKSHSPRLIKYASQISIGIPRS 81
Db 2 VLTPSPATLSTVTPGDSVSLSCRAQSISNNLHWYQOKSHSPRLIKYASQISIGIPRS 61
QY 82 FSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 127
Db 62 FSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 107

RESULT 9
PN0445

Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0445
R:Kaluzza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A:Reference number: PN0444; MUID:93138402; PMID:1339379
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-10/Domain: signal sequence #status predicted <SIG>
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 473; DB 2; Length 128;
Best Local Similarity 74.6%; Pred. No. 3e-33;
Matches 88; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
QY 11 MLFWISARGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKSHSPRLIKY 70
Db 1 LLSWIPASRGDIVLTQSPATLSTVTPGDSVSLSCRAQSISNNLHWYQOKSHSPRLIKY 60
QY 71 ASQISIGIPRSFSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 128
Db 61 ASQISIGIPRSFSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPLTFGSGTKLEI 118

RESULT 10
KYM517
Ig kappa chain precursor V region (L7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C:Accession: A01925
R:Beck, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequ
A:Reference number: A93259; MUID:81220975; PMID:6264318
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PCV>
A:Cross-references: UNIPROT:P01642; GB:V01564; GB:J00574; NID:951718; PIDN:CAA24884.1; P
A:Note: the sequence was determined from the germline gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron; th
C:Genetics: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 70.3%; Score 465; DB 1; Length 115;
Best Local Similarity 76.5%; Pred. No. 1.3e-32;
Matches 88; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
QY 1 MWFTPIILGLMLFWISARGDIVLTQSPATLSTVTPGDSVSLSCRAQIISNNLHWYQOKS 60
Db 1 MWSTPQFLVPLFLFWIPASRGDIVLTQSPATLSTVTPGDSVSLSCRAQSISNNLHWYQOKRT 60
QY 61 HESPRLLIKYASQISIGIPRSFSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPL 115
Db 61 NGSFRLIKYASQISIGIPRSFSGSGTDFLTLSINSVETEDFGMYFCQOQSNMPL 115

RESULT 11
C30502

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 62.3926 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773A-6

Perfect score: 661

Sequence: 1 MWFTPOLGLMLFMISASRG.....QQSNMPLTFGSGTKLEIKR 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_03:*
2: uniprot_09:*
3: uniprot_01:*
4: uniprot_02:*
5: uniprot_04:*
6: uniprot_05:*
7: uniprot_06:*
8: uniprot_07:*
9: uniprot_08:*
10: uniprot_10:*
11: uniprot_11:*
12: uniprot_12:*
13: uniprot_13:*
14: uniprot_14:*
15: uniprot_15:*
16: uniprot_16:*
17: uniprot_17:*
18: uniprot_18:*
19: uniprot_19:*
20: uniprot_20:*
21: uniprot_21:*
22: uniprot_22:*
23: uniprot_23:*
24: uniprot_24:*
25: uniprot_25:*
26: uniprot_26:*
27: uniprot_27:*
28: uniprot_28:*
29: uniprot_29:*
30: uniprot_30:*
31: uniprot_31:*
32: uniprot_32:*
33: uniprot_33:*
34: uniprot_34:*
35: uniprot_35:*
36: uniprot_36:*
37: uniprot_37:*
38: uniprot_38:*
39: uniprot_39:*
40: uniprot_40:*
41: uniprot_41:*
42: uniprot_42:*
43: uniprot_43:*
44: uniprot_44:*
45: uniprot_45:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	72.2	262	2	Q65211 mus musculus
2	465	70.3	115	1	KVSI_MOUSE
3	430.5	65.1	235	2	Q6GMW0 mus musculus
4	417.5	63.2	128	1	KV3K_HUMAN
5	411.5	62.3	129	1	KV3H_HUMAN
6	392	59.3	236	2	Q6GMX8 mus musculus
7	388	58.7	129	1	KV3L_HUMAN
8	387	58.5	235	2	Q6GMV9 mus musculus
9	385	58.2	236	2	Q6PIH7 mus musculus
10	385	58.2	129	1	KV3M_HUMAN
11	385	58.2	236	2	Q6GMW1 mus musculus
12	384.5	58.2	239	2	Q6NEK0 mus musculus
13	384	58.1	108	2	Q9UL83 mus musculus
14	384	58.1	236	2	Q6GMX0 mus musculus
15	380.5	57.6	109	2	Q9UL85 mus musculus
16	380	57.5	238	2	Q6GUS7 mus musculus
17	379.5	57.4	236	2	Q6PS58 mus musculus
18	379	57.3	235	2	Q6PJP2 mus musculus
19	379	57.3	240	2	Q6PIH6 mus musculus
20	378	57.2	129	1	KV1M_HUMAN
21	376.5	57.0	239	2	Q6TCD0 mus musculus
22	375.5	56.8	109	1	KV3E_HUMAN
23	374.5	56.7	236	2	Q6PIH8 mus musculus
24	372	56.3	236	2	Q723V4 mus musculus
25	370	56.0	236	2	Q6GMX9 mus musculus
26	369	55.8	115	1	KV3I_HUMAN
27	368	55.7	234	2	Q72473 mus musculus
28	368	55.7	236	2	Q6PIT5 mus musculus
29	366.5	55.4	133	1	KV2F_HUMAN
30	360.5	54.5	109	1	KV3D_HUMAN
31	359	54.3	236	2	Q6PIH4 mus musculus

32	357	54.0	134	1	KV4C_HUMAN	P06314 homo sapien
33	353.5	53.5	109	1	KV3B_HUMAN	P01620 homo sapien
34	353.5	53.5	109	2	Q9UL78	P01620 homo sapien
35	353	53.4	132	1	KV3F_MOUSE	P01658 mus musculus
36	352.5	53.3	128	1	KV3E_MOUSE	P01637 mus musculus
37	352	53.3	131	1	KV3I_MOUSE	P01631 mus musculus
38	351.5	53.2	133	1	KV4B_HUMAN	P06313 homo sapien
39	351	53.1	237	2	Q78236	Q78236 xenopus lae
40	348	52.6	108	2	Q9UL77	Q9UL77 homo sapien
41	347.5	52.6	107	2	Q96SA9	Q96SA9 homo sapien
42	346.5	52.4	109	1	KV3E_HUMAN	P01623 homo sapien
43	346.5	52.4	114	2	Q8KIF1	Q8KIF1 mus musculus
44	346	52.3	108	1	KV3S_HUMAN	P01611 homo sapien
45	346	52.3	108	2	Q9UL79	Q9UL79 homo sapien

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	262 AA.
Q65211			
AC Q65211			
DT 25-OCT-2004 (TREMBLrel. 28, Created)			
DT 25-OCT-2004 (TREMBLrel. 28, last sequence update)			
DT 25-OCT-2004 (TREMBLrel. 28, last annotation update)			
DE Anti-HIV-1 reverse transcriptase single-chain variable.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Hybridoma;			
RX MEDLINE=96211469; PubMed=8648670;			
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;			
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase			
RT by intracellular expression of single-chain variable fragments to			
RT inhibit early stages of the viral life cycle.";			
RL J. Virol. 70:3392-3400(1996).			
DR EMBL; U48716; AAB64342.1; -			
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.			
DR InterPro; IPR003599; IG_1-like.			
DR InterPro; IPR003598; IG_2-like.			
DR InterPro; IPR003596; IG_V.			
DR Pfam; PF00047; IG_2.			
DR SMART; SM00409; IG_2.			
DR SMART; SM00408; IG2; 2.			
DR SMART; SM00406; IGV; 2.			
DR PROSITE; PS00835; IG_LIKE; 2.			
DR RNA-directed DNA polymerase.			
SQ SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;			
Query Match	72.2%	Score 477;	DB 2; Length 262;
Best Local Similarity	84.3%	Pred. No. 2e-38;	7; Indels 0; Gaps 0;
Matches	91;	Conservative	10; Mismatches
QY	21	DIIVTQSPATLSVTPGDSVSLSCRASQITISNNIMHWYQOKSHSPPLTIKYSQSISGIPS	80
DB	2	DIIMTQSPATLSVTPGDSVSLSCRASQISDPLHMYQOKSHSPPLTIKYSQSISGIPS	61
QY	81	RFGSGSGTDTFLTSINSYETEDFGMYFCQGSNMPDTFGSGTKLEIKR	128
DB	62	RFGSGSGSDFTLSINSYEPDVGVYCONGHSPPLTFGAGTKLEIKR	109
RESULT 2			
KVSI_MOUSE			
ID KVSI_MOUSE			
AC P01642;			
DT 21-JUL-1966 (Rel. 01, Created)			
DT 21-JUL-1966 (Rel. 01, last sequence update)			

DT 25-OCT-2004 (Rel. 45, last annotation update)
DR Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=81220975; PubMed=6264318;
RX Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "differences between germ-line and rearranged immunoglobulin V kappa
RL coding sequences suggest a localized mutation mechanism."
RL Nature 291:668-670(1991).
CC -1- MISCELLANEOUS: There appears to be two possible splice junctions
CC at the 3' end of the intron. The alternate would code for a
CC protein lacking residues 17-19.
DR PIR; A01925; KYMSL7.
DR PDB; 1J10; X-ray; L=21-115.
DR PDB; 1J1P; X-ray; L=21-115.
DR PDB; 1J1X; X-ray; L=21-115.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-V region L7.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 >115 Complementarity-determining-3.
FT DISUFID 43 108 By similarity.
FT STRAND 24 27
FT STRAND 30 33
FT TURN 35 36
FT STRAND 39 45
FT TURN 50 51
FT STRAND 53 58
FT TURN 60 61
FT STRAND 65 69
FT TURN 70 72
FT STRAND 73 74
FT TURN 76 77
FT TURN 80 81
FT STRAND 82 87
FT TURN 88 89
FT STRAND 90 95
FT HELIX 100 102
FT STRAND 104 110
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;
Query Match 70.3%; Score 465; DB 1; Length 115;
Best Local Similarity 76.5%; Pred. No. 1,1e-37;
Matches 88; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
QY 1 MVEFTPOLGLMFWISARGDIVLTQSPATLSTPGDSVLSGCRASQIISNNLHWYQOKS 60
DB 1 MVEFTPOLGLMFWISARGDIVLTQSPATLSTPGDSVLSGCRASQIISNNLHWYQOKS 60
QY 61 HESPRLLIKYASQISGIPSRFSGSGGTDTFTLSINSVETEDFGMTFCQGSNSMP 115
DB 61 HESPRLLIKYASQISGIPSRFSGSGGTDTFTLSINSVETEDFGMTFCQGSNSMP 115
RESULT 3
Q6GMMO PRELIMINARY; PRT; 235 AA.
AC Q6GMMO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DR 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA TISSUE=Spleen.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman P.J., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywnicki M.I., Skaleka U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RA TISSUE=Spleen;
RC Strausberg R.,
RL SMDL; BC073792; AAH73792.1; -.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;
Query Match 65.1%; Score 430.5; DB 2; Length 235;
Best Local Similarity 66.9%; Pred. No. 6,1e-34;
Matches 83; Conservative 19; Mismatches 21; Indels 1; Gaps 1;
QY 6 QILGLMFWISARGDIVLTQSPATLSTPGDSVLSGCRASQIISNNLHWYQOKS 65
DB 6 QILGLMFWISARGDIVLTQSPATLSTPGDSVLSGCRASQIISNNLHWYQOKS 65
QY 66 LIIKYSQGISGIPSRFSGSGGTDTFTLSINSVETEDFGMTFCQGSNSMP 124
DB 66 LIIKYSQGISGIPSRFSGSGGTDTFTLSINSVETEDFGMTFCQGSNSMP 124
QY 125 EIKR 128
DB 125 EIKR 128
RESULT 4
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC KV3K_HUMAN;
DT P06311;

DT	01-JAN-1968	(Rel. 06, Created)
DT	01-JAN-1968 <td>(Rel. 06, Last sequence update)</td>	(Rel. 06, Last sequence update)
DT	15-JUL-1999 <td>(Rel. 38, Last annotation update)</td>	(Rel. 38, Last annotation update)
DE	Ig kappa chain V-II region	IARC/BL41 precursor.
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxId=9606;	
RN	SEQUENCE FROM N.A.	
RP	MEDLINE=86041852; PubMed=2997711;	
RA	Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;	
RT	"Human immunoglobulin kappa light chain genes of subgroups II and III."	
RL	Nucleic Acids Res. 13:6499-6513 (1985).	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation at	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@ib-sib.ch).	
CC	-----	
DR	EMBL; Z00021; CA77316.1; -	
DR	PIR; A01899; K3H041.	
DR	HSSP; P01625; IIEQ.	
DR	GO; GO:0005576; C:extracellular; NAS.	
DR	GO; GO:0003823; F:antigen binding; NAS.	
DR	GO; GO:0006955; P:immune response; NAS.	
DR	InterPro; IPRO07110; IG-like.	
DR	InterPro; IPRO03596; IG_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM0406; IGV; 1.	
DR	PROSITE; PS0835; IG LIKE; 1.	
KW	Immunoglobulin V region; Signal.	
FT	SIGNAL	1
FT	CHAIN	21 128
FT	DOMAIN	21 43
FT	DOMAIN	44 54
FT	DOMAIN	55 69
FT	DOMAIN	70 76
FT	DOMAIN	77 108
FT	DOMAIN	109 117
FT	DOMAIN	118 128
FT	DISULFID	43 108
FT	NON TER	128 128
SO	SEQUENCE	128 AA; 14070 MW; C68957F0E3B9012 CXC64;
Query Match	63.2%; Score 417.5; DB 1; Length 128;	
Best Local Similarity	64.3%; Pred. No. 5.7e-33;	
Matches	81; Conservative 20; Mismatches 24; Indels 1; Gaps 1;	
OY	4 TP-QILGLMTLWISASRDIVLTQSPALSTLTPGDSVSLSCRAQIISNNLHWYQOKSHE 62	
Db	3 TPQQLFLLLLMLLPDTTSEIVLTQSPGLTSLSPGSATLSRAQSVSNLAWYQOKRGQ 62	
OY	63 SPRLILIKVASQISIGIPRFSGSGSGDTFTLSINSVETEDFGMYFCQOQSNEMPTLPGSGT 122	
Db	63 SPRLILIRASRANGIPDRFSGSGSGDPTLILISLREPDVAIVYCCQYTSPTTGGCT 122	
OY	123 KLEIKR 128	
Db	123 KLEIKR 128	
RESULT 5		
KV3H_HUMAN	STANDARD;	PRT; 129 AA.
AC	P04207;	
DT	20-MAR-1987 (Rel. 04, Created)	
DT	01-NOV-1980 (Rel. 16, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	

DE	Ig kappa chain V-II region CLL precursor (Rheumatoid factor).
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=86177570; PubMed=3083417;
RA	Jirik F.R., Soxe J., Pong S., Heitzmann U.G., Curod J.G., Chen P.P.,
RT	Goulden R., Carson D.A.;
RT	"Cloning and sequence determination of a human rheumatoid factor
RL	light-chain gene.";
CC	Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC	or send an email to license@ebi.ac.uk).
CC	-----
DR	EMBL; M12740; AAA58992.1; --
DR	HSSP; P01625; ILVE.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IgV_1.
DR	PROSITE; PS50835; Ig_LIKE; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
SO	SEQUENCE
Query Match	Best Local Similarity 62.3%; Score 411.5; DB 1; Length 129;
Matches	77; Conservative 24; Mismatches 22; Indels 1; Gaps 1;
DQ	6 QIIGLMFMFWISASRGKDIVLTQSPTATLSVTGSDSVSLSCRASQTILSNMLHWYQOKSHSPR 65
DB	6 QLLEFLILLMLPDITGEIVMTQSPATLSVSGERARTLSCRASQSVSNLLAWYQOKRGQPPR 65
DQ	6 LLIKYASQSIISGIPSRPSGSGSGTDPTLINSVETEDFGMYFCQGSNSM-PITPGSGTKL 124
DB	66 LLIIAGASTRATGIPARFSGSGSGTEFTLTISRLQSEDFAVYYCOQYNMWPMPWGQGTRV 125
DQ	125 EIKR 128
DB	126 EIKR 129
RESULT 6	
O6GMX8	PRELIMINARY; PRT; 236 AA.
AC	O6GMX8;
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DS	Hypothetical protein..
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Primary B-Cells;
 RA Strausberg R.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073764; AAH73764.1; -
 DR InterPro: IPR003599; IG_-
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF07654; Cl-sec; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein_
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
 Query Match 59.3%; Score 392; DB 2; Length 236;
 Best Local Similarity 60.2%; Pred. No. 3.6e-30;
 Matches 74; Conservative 25; Mismatches 24; Indels 0; Gaps 0;
 QY 6 OILGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPR 65
 DB 8 QILGLLMLPPGSGCDIQMTQSPBSVASVGDRTYITCRASQGISLWAWYQOKPGKAPK 67
 QY 66 LLIKYASQSIISGIPSRFSGSGGTDFLTLSINVTEDPFQMYFCQGSNSMPLTFGSGTKLE 125
 DB 68 LLITAASSLQSGVPSRFSGSGGTDFLTLSLQPEDPFAYVYCOQANSFPFTGPGTKVD 127
 QY 126 IKR 128
 DB 128 IKR 130
 RESULT 7
 KVAL_HUMAN STANDARD; PRT; 129 AA.
 ID KVAL_HUMAN
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region HAH precursor.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=68171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.,
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: The protein is one of the surface immunoglobulin M
 autoantibodies expressed in patients with chronic lymphocytic
 leukemia.
 CC PIR; P10022; KJHDA.
 DR HSSP; P01625; 1EEQ.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129
 FT DOMAIN 21 43
 FT DOMAIN 44 55
 FT DOMAIN 56 70
 FT DOMAIN 71 77
 FT DOMAIN 78 109
 FT DOMAIN 110 118
 FT DOMAIN 119 129
 FT DISUFID 43 109
 FT NON_TER 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
 Query Match 58.7%; Score 388; DB 1; Length 129;
 Best Local Similarity 60.6%; Pred. No. 4.4e-30;
 Matches 77; Conservative 22; Mismatches 26; Indels 2; Gaps 2;
 QY 4 TP-OILGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSH 61
 DB 3 TPAQLFLMLWLPDTGTGIVLTQSPGTLSLSPGERATLSCRASQGVSSSYLWAWYQOKSG 62
 QY 62 ESPRLIKYASQSIISGIPSRFSGSGGTDFLTLSINVTEDPFQMYFCQGSNSMPLTFGSG 121
 DB 63 QAPRLIHYGASSRATGIPSRFSGSGGTDFLTLSLQPEDPFAYVYCOQYGTSPRTFGGQ 122
 QY 122 TKLEIKR 128
 DB 123 TKLEIKR 129
 RESULT 8
 OGKGV9
 ID OGKGV9
 AC OGKGV9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strusberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073793; AAH73793.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 235 AA; 25646 MW; DF32B560BAD12E4B CRC64;

Query Match 58.7%; Score 388; DB 2; Length 235;
 Best Local Similarity 61.4%; Pred. No. 8.8e-30;
 Matches 78; Conservative 20; Mismatches 27; Indels 2; Gaps 2;
 QY 4 TP-OLGLMFWISASRGDIVLTOSPATLSTVPDGSVSLSCASASQII-SNNLHWYQKSH 61
 DB 3 TPAQLFLPLMLLPITGIVLTQSPGTLSLSPGERAAALSCASQSVNSKYLAWYQKPG 62
 QY 62 ESPRLILIKYASQISGIPSRFSGSGGTFTLINSVERTEDFGMYFCQGSNSWPLTFGSG 121
 DB 63 QAPRLMLVAASIRATGIPDRFSGSGGTFTLITRLSEDFALYFCQGYGSPITFGSG 122
 QY 122 TKLEIKR 128
 DB 123 TKVEIKR 129

RESULT 9
 ID Q6PIH7 PRELIMINARY; PRT; 236 AA.
 AC Q6PIH7;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strusberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034141; AAH34141.1; -.
 DR HSP; P01607; IAR2.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106661213F CRC64;

Query Match 58.5%; Score 387; DB 2; Length 236;
 Best Local Similarity 61.8%; Pred. No. 1.1e-29;
 Matches 76; Conservative 20; Mismatches 27; Indels 0; Gaps 0;
 QY 6 QILGLMFWISASRGDIVLTOSPATLSTVPDGSVSLSCASQII-SNNLHWYQKSHESR 65
 DB 8 QILGLLMLLPARCDIQLTQSPGLSPFLSASVGRVITCRASQGISSTYLAWYQKPKAPN 67
 QY 66 LLIKVASQISGIPSRFSGSGGTFTLINSVERTEDFGMYFCQGSNSWPLTFGSGTKLE 125
 DB 68 LLIYVAASITQSGVSPSRFSGSGGTFTLITISLQPEDPATYICQQLNSPPTFGSGTKVE 127
 QY 126 IKR 128
 DB 128 IKR 130

RESULT 10
 ID KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=8817107; PubMed=3127527;
 Kips T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
 J. Exp. Med. 167:840-852(1988).

CC -1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.

DR HSP; P01625; IIEQ.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129

FT DOMAIN 21 43

FT DOMAIN 44 55

FT DOMAIN 56 70

FT DOMAIN 71 77

FT DOMAIN 78 109

FT DOMAIN 110 118

FT DOMAIN 119 129

FT DISULFID 43 109

FT NON TER 129 129

SO SEQUENCE 129 AA; 14070 MW; 7395528BA2B74D6 CRC64;

Query Match 58.2%; Score 385; DB 1; Length 129;
 Best Local Similarity 60.6%; Pred. No. 8.6e-30;

Matches 77; Conservative 21; Mismatches 27; Indels 2; Gaps 2;

QY 4 TP-QILGLMFWISASRGDIYLTQSPATISVTPGDSVSLSCASQIISNN-LHWYQKSH 61

DB 3 TPQQLFLFLMLPDTTGTIVLTQSPETLSLSPERATLSCASQVSSSYLAWYQKPG 62

QY 62 ESRRLLIKYASQISIGIPRSFGSGSGTFTLSINSVETEDFCGMVFCQOQNSMPLTFGSG 121

DB 63 QARLLIYKASRATGIPDFSGSGSGTFTLTISRLPEKDFAYVYCOQYQSSPMTFGG 122

QY 122 TKLEIKR 128

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

DB 123 TKVEIKR 129

Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pallen J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073791; AAH73791.1; -

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IGV; 2.

DR SMART; SM00407; IGV; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR Hypothetical protein.

KW SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC37 CRC64;

Query Match 58.2%; Score 385; DB 2; Length 236;
 Best Local Similarity 59.3%; Pred. No. 1.7e-29;

Matches 73; Conservative 24; Mismatches 26; Indels 0; Gaps 0;

QY 6 QILGLMFWISASRGDIYLTQSPATISVTPGDSVSLSCASQIISNN-LHWYQKSHESPR 65

DB 8 QILGLLMLPGRCAIQMTQSPSSLSASVGRVITTCRASQGISNDLGMWYQKPGKAPK 67

QY 66 LLIKVASQISIGIPRSFGSGSGTFTLSINSVETEDFCGMVFCQOQNSMPLTFGSGTKLE 125

DB 68 LLIVAASSLSQSGVPSRFSFGSGSGTFTLTISLQPEDFAVYVYCLQDYNPMTFGSGTKVE 127

QY 126 IKR 128

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

DB 128 IKR 130

RESULT 11
 Q6GMW1 PRELIMINARY; PRT; 236 AA.

AC O6GMW1; (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RESULT 12
 Q8NEKO PRELIMINARY; PRT; 239 AA.

AC Q8NEKO; (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 SQ [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030814; AAH30814.1; -.
 DR PIR; S23638; S23638.
 DR PIR; S34091; S34091.
 DR PIR; S40342; S40342.
 DR PIR; S40357; S40357.
 DR HSSP; P01834; I172.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; Cl-sec; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
 Query Match 58.2%; Score 384.5; DB 2; Length 239;
 Best Local Similarity 57.8%; Pred. No. 28-29;
 Matches 74; Conservative 17; Mismatches 32; Indels 5; Gaps 1;
 QY 6 QILGMLTWISAKRDIVLTOSPATLSTPGDSVLSGRASGIT-----SNLTHYQOKS 60
 DB 6 QILGMLTWISAKRDIVLTOSPATLSTPGDSVLSGRASGIT-----SNLTHYQOKS 65
 QY 61 HESPLRLIKYASQSISGIPRSFGSGSGGTFTLSINVTEDFGMYFCQGSNWPRTGCS 120
 DB 66 GQSPDLIYLYGSNRASGVDPDRFGSGSGGTFTLTKISKYEAADVIGIYCCQGLQTPQTRFQ 125
 QY 121 GTKLEIKR 128
 DB 126 GTKVEIKR 133
 RESULT 13
 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
 AC Q9UL83;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus",
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035031; AAD56267.1; -.

DR PIR; B30609; B30609.
 DR PIR; C30609; C30609.
 DR PIR; D30609; D30609.
 DR PIR; S34098; S34098.
 DR PIR; S34099; S34099.
 DR HSSP; P01625; I1VE.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A928BA96EEA CRC64;
 Query Match 58.1%; Score 384; DB 2; Length 108;
 Best Local Similarity 64.8%; Pred. No. 8-30;
 Matches 70; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
 QY 21 DIVLTOSPATLSTPGDSVLSGRASGITISNNLTHYQOKSHSPRLIKYASQSISGIPS 80
 DB 1 EIVMTOSPATLSTPGDSVLSGRASGITISNNLTHYQOKSHSPRLIKYASQSISGIPS 60
 QY 81 RFGSGSGTDFLTLSINVTEDFGMYFCQGSNWPRTGSGTKLEIKR 128
 DB 61 RFGSGSGTDFLTLSINVTEDFGMYFCQGSNWPRTGSGTKLEIKR 108
 RESULT 14
 ID Q6GKX0 PRELIMINARY; PRT; 236 AA.
 AC Q6GKX0;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshitake S., Carrinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073775; AAH73775.1; -.
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.

Search completed: May 25, 2005, 15:56:03
Job time : 63.3926 secs

DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-set; 1.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.
DR PROSITE: PSS0290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 58.1%; Score 384; DB 2; Length 236;
Best Local Similarity 59.3%; Pred. No. 2.2e-29;
Matches 73; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 6 QILGLMLFWISASRGDIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPR 65
DB 8 QILGLMLMKGARCDIQMTQSPSSLSASVGDRTITCRASQININNYQALPKAPR 67
QY 66 LLIKVASQSIGIPSPRSGSGGTPTLSINSVETEDFGMYFCQGSNSWPLTFGSGTKLE 125
DB 68 LLIIYAASSIQSGVPSRFSGSGGTPTLTITSLRPDPFATYYCQGSYNIPLTFGCGTNVE 127

QY 126 IKR 128
DB 128 IKR 130

RESULT 15
O9UL85 PRELIMINARY; PRT; 109 AA.

AC O9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035029; AAD56265.1; -.
DR PIR; D30609; D30609.
DR HSSP; P01625; 1EK3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACC CRC64;

Query Match 57.6%; Score 380.5; DB 2; Length 109;
Best Local Similarity 67.9%; Pred. No. 2e-29;
Matches 74; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 21 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPRLLIKVASQSIGIPS 80
DB 1 EIVMTOSPATLSVSPERATLSVSCWASQISSNLAWYQKPGQAPRLIIYGASTRAATGIPA 60
QY 81 RFGSGSGGTPTLSINSVETEDFGMYFCQGSNSW-PLTFGSGTKLEIKR 128
DB 61 RFGSGSGGTPTLTITSLSGSEDPATYHCCQYNSWPLTFGSGTKVEIKR 109

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3D8 heavy chain variable region
 XX

SQ Sequence 133 AA;

Query Match 100.0%; Score 684; DB 6; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1e-54; Mismatches 0; Gaps 0;
 Matches 133; Conservative 0; Indels 0;

QY 1 MNFGSLIFLVYLKGVQCEVKVBSGGGLVFKPGASLKLSCAAGFTFSNYGMSWVRQTS 60
 DB 1 MNFGSLIFLVYLKGVQCEVKVBSGGGLVFKPGASLKLSCAAGFTFSNYGMSWVRQTS 60
 QY 61 DKRLWVASISGGGSTFYADNVKGRFTISRANKNTLYLQMSLKSSEDTALYYCARDDL 120
 DB 61 DKRLWVASISGGGSTFYADNVKGRFTISRANKNTLYLQMSLKSSEDTALYYCARDDL 120
 QY 121 FNMGGTTLTVSS 133
 DB 121 FNMGGTTLTVSS 133

RESULT 2

ABG76924 standard; protein; 138 AA.

AC ABG76924;
 DT 05-NOV-2002 (first entry)
 XX

DE Mouse 3D6 VH protein.

XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
 KW variable region complementarity determining region; 3D6; 10D5;
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
 KW Abeta.

XX Mus musculus.

XX WO200246237-A2.

XX 13-JUN-2002.

XX 06-DEC-2001; 2001WO-US046587.

XX 06-DEC-2000; 2000US-0251892P.

XX (NEUR-) NEURALAB LTD.

XX (AMHP) WYETH.

XX Basi G, Saldanha J, Yednock T;

XX WPI; 2002-519658/55.

XX N-PSDB; ABS59427.

XX Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.

XX Claim 68; Fig 2; 171pp; English.

XX The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.

CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention
 XX

SQ Sequence 138 AA;

Query Match 89.3%; Score 610.5; DB 5; Length 138;
 Best Local Similarity 87.0%; Pred. No. 5.6e-48;
 Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVKVBSGGGLVFKPGASLKLSCAAGFTFSNYGMSWVRQTS 60
 DB 1 MNFGSLIFLVYLKGVQCEVKVBSGGGLVFKPGASLKLSCAAGFTFSNYGMSWVRQTS 60
 QY 61 DKRLWVASISGGGSTFYADNVKGRFTISRANKNTLYLQMSLKSSEDTALYYCARDDL 120
 DB 61 DKRLWVASISGGGSTFYADNVKGRFTISRANKNTLYLQMSLKSSEDTALYYCARDDL 120
 QY 121 FNMGGTTLTVSS 133
 DB 121 YSGSSDYWGQTTTVSS 138

RESULT 3

ADR88408 standard; protein; 138 AA.

AC ADR88408;

DT 16-DEC-2004 (first entry)

DE Murine 3D6 immunoglobulin heavy chain variable region SEQ ID NO:4.

XX 3D6; heavy chain variable region; immunoglobulin;
 KW complementarity determining region; CDR; 10D5; variable framework region;
 KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
 KW Alzheimer's disease.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..19
 FT /label= signal peptide
 FT 20..138
 FT /label= mature protein

XX WO2004080419-A2.

XX 23-SEP-2004.

XX 12-MAR-2004; 2004WO-US007503.

XX 12-MAR-2003; 2003US-00388389.

XX (NEUR-) NEURALAB LTD.

XX (AMHP) WYETH.

XX Basi G, Saldanha JW, Yednock T;

XX WPI; 2004-668880/65.

XX N-PSDB; ADR88407.
 PT New humanized antibodies that recognize beta amyloid peptides, useful for
 PT preventing or treating amyloidogenic diseases, such as Alzheimer's
 PT disease.

XX Claim 2; SEQ ID NO 4; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy
 CC chain. The humanised immunoglobulin light or heavy chain comprises:
 CC variable region complementarity determining regions (CDR's) from the 3D6

immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 138 amino acids fully defined in the specification (ADR88408); or from the 1005 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or heavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 or 10D5 light or heavy chain variable region sequence, where the framework residue is a residue that non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR-intersecting residue or a residue participating in the VL-VH interface. An antibody of the invention has neuroprotective and neurotropic activity, and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as Alzheimer's disease. The variable region sequence is useful in producing a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin chain, or its domain. The present sequence represents the murine 3D6 immunoglobulin heavy chain variable region.

Sequence 138 AA;

Query Match 89.1%; Score 609.5; DB 8; Length 138;
Best Local Similarity 87.0%; Pred. No. 6,9e-48;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60
DB 1 MNFGSLIFLVVLKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQWSSLSKSDTALYYCARDL 120
DB 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQWSSLSKSDTALYYCARDL 120
QY 121 FN-----WGQGTTLTVSS 133
DB 121 YSGSSDYWGQGTTVTVSS 138

RESULT 4
ABG74247
ID ABG74247 standard; protein; 139 AA.

AC ABG74247;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3E11 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;
XX immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D6; 4D4;
XX 3E11; prostate-specific membrane antigen; zeta signalling chain;
XX CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
XX small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

PN US2002132983-A1.

PD 19-SEP-2002.

PP 10-DEC-2001; 2001US-00006773.

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Jungmans RP;

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16573.

XX New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX Disclosure; Page 17; 35pp; English.

XX The invention relates to a chimeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody 3E11 heavy chain variable region

Sequence 139 AA;

Query Match 86.3%; Score 590; DB 6; Length 139;
Best Local Similarity 83.5%; Pred. No. 4.2e-46;
Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60
DB 1 MNFGSLIFLVVLKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQWSSLSKSDTALYYCARDL 119
DB 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQWSSLSKSDTALYYCARDL 119
QY 120 -----LFWGQGTTLTVSS 133
DB 120 SVGCWPFATWGQGTTLTVSSA 139

RESULT 5
AAO29869
ID AAO29869 standard; protein; 462 AA.

AC AAO29869;

DT 27-AUG-2003 (first entry)

DE Mouse anti-human DR5 antibody (TR8-8) heavy chain.

XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
XX inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
XX Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
XX multiple sclerosis; graft-versus-host disease; arteriosclerosis; actina;
XX Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
XX Crohn's disease; diabetes mellitus; antibody; mouse.

OS Mus sp.

PN WO2003037913-A2.

PD 08-MAY-2003.

PP 01-NOV-2002; 2002WO-US035333.

PR 01-NOV-2001; 2001US-0346402P.

XX (UABR-) UAB RES FOUNDED.

XX Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;

DR WPI, 2003-441350/41.
 XX N-PDB; AAL60477.
 XX
 PT New purified antibody that specifically binds a TNF-related apoptosis-
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
 PT rheumatoid arthritis.
 XX
 PS Example 16; Page 224-225; 251pp; English.
 XX
 CC The invention relates to an antibody that specifically binds a tumour
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 CC DR4 or DR5. Antibodies of the invention are useful for selectively
 CC inducing apoptosis in target cells expressing DR4, for inhibiting
 CC proliferation of target cells expressing DR4 or for treating cancer,
 CC inflammatory disease or autoimmune disease in a subject e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
 CC glomerular nephritis. The present sequence is mouse anti-human DR5
 CC antibody (TRA-8) heavy chain
 CC
 SQ Sequence 462' AA:
 Query Match 83.3%; Score 569.5; DB 6; Length 462;
 Best Local Similarity 81.9%; Pred. No. 1.2e-43;
 Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;
 QY 1 MNFGSLIFLVVLKGVQCEVKVSGGLVPRGASLKISCAASGFTPSNYGMSWVRQTS 60
 DB 1 MNFGSLIFLVVLKGVQCEVMLVESGGGLVPRGSLKISCAASGFTPSYVMSWRQTP 60
 QY 61 DKRLWVASISSGGSTFPYADVNGKRPFTISRBNKNTLYLQMSLSKSEPTALYYCAR--D 118
 DB 61 EKRLWVAITISSGGSTYYPDVSVKGRFTISRDNKNTLYLQMSLSKSEPTAMYYCARRGD 120
 QY 119 DLFN--WGQGTTLTVSS 133
 DB 121 SMITTDYWGQGTTLTVSS 138
 RESULT 6
 ADJ79787
 ID ADJ79787 standard; protein; 462 AA.
 XX
 AC ADJ79787;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE TRA-8 antibody heavy chain.
 XX
 KM nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
 KM antiatherogenic; antiinflammatory; antidiabetic; haemostatic;
 KM neuroprotective; antifertility; immunosuppressive; dermatological;
 KM antianaemic; antitrematic; antiarthritic; thyromimetic; apoptosis;
 KM proliferation;
 KM tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
 KM TRAIL; synovial cell; lymphocyte; neutrophil;
 KM systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
 KM graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
 KM Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
 KM autoimmune hemolytic anemia; sterility; myasthenia gravis;
 KM multiple sclerosis; Basedow's disease; thrombocytopenia;
 KM thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
 KM asthma, atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
 KM glomerular nephritis; hypoplastic anemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003038043-A2.
 XX
 PD 08-MAY-2003.
 XX

PF 25-OCT-2002; 2002MO-US034420.
 XX
 XX 01-NOV-2001; 2001US-0346402P.
 PR 24-JUN-2002; 2002US-0391478P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
 PI Lobuglio AF, Buchsbaum DJ;
 XX
 DR WPI, 2003-421518/39.
 XX
 PT Inducing apoptosis and inhibiting proliferation of target cells
 PT expressing DR5, by contacting the target cell with an antibody that binds
 PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
 PT agents.
 XX
 PS Example 16; SEQ ID NO 23; 274pp; English.
 XX
 CC The invention relates to a method of selectively inducing apoptosis in
 CC and inhibiting (M1) proliferation of target cells expressing DR5,
 CC comprising contacting the cell with an antibody that specifically binds
 CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
 CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
 CC vitro apoptosis-inducing activity in the cell expressing DR5, and
 CC contacting the cell with one or more therapeutic agents. M1 is useful for
 CC inducing apoptosis in target cell and inhibiting proliferation of target
 CC cell expressing DR5, where the target cell is an abnormally proliferating
 CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
 CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
 CC cell. M2 is useful for treating a subject having inflammatory and
 CC autoimmune diseases. The inflammatory or autoimmune disease are selected
 CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
 CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
 CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
 CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
 CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
 CC protein used in the method of the invention.
 CC
 SQ Sequence 462 AA:
 Query Match 83.3%; Score 569.5; DB 7; Length 462;
 Best Local Similarity 81.9%; Pred. No. 1.2e-43;
 Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;
 QY 1 MNFGSLIFLVVLKGVQCEVKVSGGLVPRGASLKISCAASGFTPSNYGMSWVRQTS 60
 DB 1 MNFGSLIFLVVLKGVQCEVMLVESGGGLVPRGSLKISCAASGFTPSYVMSWRQTP 60
 QY 61 DKRLWVASISSGGSTFPYADVNGKRPFTISRBNKNTLYLQMSLSKSEPTALYYCAR--D 118
 DB 61 EKRLWVAITISSGGSTYYPDVSVKGRFTISRDNKNTLYLQMSLSKSEPTAMYYCARRGD 120
 QY 119 DLFN--WGQGTTLTVSS 133
 DB 121 SMITTDYWGQGTTLTVSS 138
 RESULT 7
 AAU72801
 ID AAU72801 standard; protein; 464 AA.
 XX
 AC AAU72801;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE TRA-8 heavy chain.
 XX
 KM Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
 KM TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
 KM

```

KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
XX Mus musculus.
XX
XX WO200183560-A1.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014151.
XX
XX 02-MAY-2000; 2000US-0201344P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
XX WPI; 2002-049338/06.
XX
XX N-PSDB; AAS97062.
XX
XX Novel antibody specific for tumor necrosis factor-related apoptosis-
XX inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
XX Claim 26; Page 198-199; 229pp; English.
XX
XX The invention describes a novel antibody which recognizes a tumour
XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
XX DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
XX activity to a cell expressing DR5 in vivo. It is also useful for
XX preparing a therapeutic for selective apoptosis of abnormal or
XX dysregulated cells, and for inhibiting cell proliferation in a cell,
XX preferably a human breast, ovary, colon, haematopoietic, prostate,
XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
XX also be administered e.g. paclitaxel, taxol or cycloheximide. The
XX antibody is used to treat an autoimmune disease, systemic lupus
XX erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
XX host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
XX Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
XX haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
XX Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
XX disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, rejection after organ transplantation,
XX and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
XX breast tissue. Peptides used to design primers for isolating heavy and
XX light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
XX shown in AAU72799 and AAU72800
XX
XX Sequence 464 AA;
XX
XX Query Match 83.3%; Score 569.5; DB 5; Length 464;
XX Best Local Similarity 81.9%; Pred. No. 1.2e-43;
XX Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;
XX
XX 1 MNFGSLFLVLYLVKGVCEVYVSGGGLVYRGSALSLSCAAGFTSSNYGMSVNRQTS 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MNFGSLFLVLYLVKGVCEVYVSGGGLVYRGSGLSLSCAAGFTSSNYGMSVNRQTP 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX 61 DKRLWVYVSISSGGSDTFYADNVKGRFTISRENANRNTLYLQMSLKSDEDTALYYCAR--D 118
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 EKRLWVATISSGGSYTYTPDSVYKRFITISDNMAQNTLYLQMSLSRSEDITAMYYCARAGD 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX 119 DLFN--WGCGTTLTVSS 133
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX 121 SMITTDYWGCGTTLTVSS 138
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX RESULT 8
XX ABB979730
XX ID ABB979730 standard; protein; 144 AA.

```

XX ABB79730;
AC
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.
XX
KM Streptococcus mutans; monoclonal antibody; Mab; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
XX immunotherapy; therapy.
OS
Mus musculus.
XX
FN US2002068066-A1.
XX
PD 06-JUN-2002.
XX
PF 15-JUN-2001; 2001US-00881823.
XX
PR 20-AUG-1999; 99US-00378577.
XX
PA (SHW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
DR WPI: 2002-565838/60.
DR N-Psdb; ABN84611.

Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of cariogenic organisms.

Claim 14; Fig 3B; 30pp; English.

The present sequence is the protein sequence of the heavy chain variable region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds specifically to the surface antigens of cariogenic type c Streptococcus mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC HB 12558) hybridoma cells. In an example from the invention, chimeric monoclonal antibody TBP was produced comprising SWLA3 variable regions and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental caries in humans. The antibodies engage the effector apparatus of the human immune system when they bind to cariogenic organisms, resulting in their destruction. The chimeric antibodies may be produced in edible plants, in transgenic animals, or in chicken eggs for oral ingestion

Sequence 144 AA;

Query Match 81.8%; Score 559.5; DB 5; Length 144;
Best Local Similarity 76.1%; Pred. No. 2.7e-43;
Matches 108; Conservative 15; Mismatches 10; Indels 9; Gaps 1

CY 1 MNFGSLFLVLTKGVOCCEKVVSGGLYKPGASLKLSCAAGFTFSAIVGMNVROTSS 60
DB 1 MDFGIHLFLVLTKGVOCCEKVVSGGLYKPGASLKLSCAAGFTFSAIVGMNVROTSS 60
CY 61 DKRLFWVASISGGSTFYADNVGRFTISRPMANKNTLYIQWSSLSKEPTALYYCARDP- 119
DB 61 EKRLFWVASISGGSTFYADNVGRFTISRPMANKNTLYIQWSSLSKEPTALYYCARDP 120
CY 120 -----LFNMGGCTTLTVSS 133
DB 121 SYGSYYTAMDYMGCGTSTVTSS 142

RESULT 9
AAW57592

ID AAW57592 standard; protein; 137 AA.
 XX
 AC AAW57592;
 XX
 DT 03-SEP-1998 (first entry)
 XX
 DE Chimeric antibody against hPTRP H chain V region SEQ ID NO:57.
 XX
 KM Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;
 KM L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KM hypophosphemia; pathogen; vitamin D resistance; V region; C region;
 KM humanised.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO9813388-A1.
 XX
 PD 02-APR-1998.
 XX
 PF 24-SEP-1997; 97MO-JP003382.
 XX
 PR 26-SEP-1996; 96JP-00255196.
 PR 24-JUL-1997; 97JP-00214168.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Sato K, Wakahara Y, Yabuta N;
 XX
 DR WPI; 1998-230640/20.
 DR N-PSDB; AAV24232.
 XX
 PT New chimeric antibodies against human parathormone related peptide(s) -
 PT useful for, e.g. treatment of hypercalcaemia and other disorders caused
 PT by malignant neoplasm(s).
 XX
 PS Claim 52; Page 120-121; 182pp; Japanese.
 XX
 CC New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric L
 CC and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They may
 CC also be used for treatment of hypophosphemia such as that due to
 CC pathogens or to vitamin D resistance

AAW89625
 ID AAW89625 standard; protein; 137 AA.
 XX
 AC AAW89625;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE Mouse humanised antibody #23-57-137-1 heavy chain protein.
 XX
 KM Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KM inhibitor; humanised.
 XX
 OS Mus sp.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= signal
 FT 20..137
 XX
 PN WO9851329-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 13-MAY-1998; 98MO-JP002116.
 XX
 PR 15-MAY-1997; 97JP-00125505.
 PR 18-JUL-1997; 97JP-00194445.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Sato K, Tunesari T, Ishii K;
 XX
 DR WPI; 1999-070101/06.
 DR N-PSDB; AAX00092.
 XX
 PT Inhibitors of binding of parathyroid hormone related peptide to its
 PT receptor - useful for, e.g. treatment of cachexia arising from cancer or
 PT other diseases.
 XX
 PS Example 2; Page 82; 125pp; Japanese.
 XX
 CC The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an active
 CC component. This substance may be an antagonist to the receptor, or an
 CC antibody (preferably monoclonal) or antibody fragment, recognising PTHrP.
 CC The antibody is preferably humanised or chimeric. The present invention
 CC also describes a humanised antibody prepared by hybridoma 23-57-137-1
 CC (FERM BP-5631). The composition is used for the treatment of cachexia
 CC arising in connection with diseases such as cancer, thereby improving the
 CC quality of life of the patient. The present sequence represents mouse
 CC humanised antibody heavy chain from #23-57-137-1 from the present
 CC invention
 XX
 SQ Sequence 137 AA;
 XX
 Query Match 81.7%; Score 559; DB 2; Length 137;
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;
 XX
 QY 1 MNFGSLIFLVVLKGVQCEVKVSGGGLVYKPGASLKLKSCAAGTFFSNYGMWVRQTS 60
 DB 1 MNFGSLIFLVVLKGVQCEVKVSGGGLVYKPGASLKLKSCAAGTFFSNYGMWVRQTS 60
 QY 61 DKRLEWVASISGGSDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSEDTALYYCARDDL 120
 DB 61 DKRLEWVASISGGSDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSEDTALYYCARDDL 120
 QY 121 FN----WGQGTTLTVSS 133
 DB 121 MTFAYWGGGTLTVVSA 137
 QY 121 MTFAYWGGGTLTVVSA 137
 DB 121 MTFAYWGGGTLTVVSA 137

RESULT 11
 ID AAY77513
 AC AAY77513 standard; protein; 137 AA.
 XX
 XX AAY77513;
 DT 26-APR-2000 (first entry)
 DE Mouse antibody H chain V region.
 XX
 XX Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.
 XX
 XX Mus musculus.
 OS
 PN WO200000219-A1.
 PD 06-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-JP003433.
 XX
 XX 26-JUN-1998; 98JP-00180143.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Sato K, Tsunenari T;
 PI
 XX
 DR MPI: 2000-117115/10.
 DR N-PSDB; AA258913.
 XX
 XX
 PT Treatment of hypercalcaemic crisis with a substance inhibiting binding of
 PT parathyroid hormone related peptide to its receptor.
 XX
 XX Example 2; Page 96-97; 120pp; Japanese.
 XX
 XX The invention relates to a method of treatment of hypercalcaemic crisis. A
 CC composition for the treatment of hypercalcaemic crisis contains as active
 CC component a substance which inhibits the binding of parathyroid hormone
 CC related peptide (PTHrP) to its receptor. The inhibitor is used for the
 CC treatment of hypercalcaemic crisis, such as that associated with a
 CC malignant tumour
 CC
 CC
 SQ Sequence 137 AA;

Query Match 81.7%; Score 559; DB 3; Length 137;
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVAVVSSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60
 DB 1 MNFGSLIFLVVLKGVQCEVAVVSSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60
 QY 61 DKRLMVAVATISSGGSTFYADVVKGRFTISRANAKNTLYLQMSLKSEDTALYYCARDDL 120
 DB 61 DKRLMVAVATISSGGSTFYADVVKGRFTISRANAKNTLYLQMSLKSEDTALYYCARDDL 120
 QY 121 FN---WGQGTLLTVSS 133
 DB 121 MTFYFVWGQGTLLTVSA 137

RESULT 12
 ID AAG67102
 AC AAG67102 standard; protein; 137 AA.
 XX
 XX AAG67102;
 DT 13-NOV-2001 (first entry)
 DE Amino acid sequence of a murine antibody directed against PTH.
 XX
 XX Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;
 KW septicemia; injury; muscular dystrophy; cytokine; interleukin-6;

KW granulocyte colony stimulating factor; interleukin-11;
 KW leukemia inhibitory factor; weight loss.
 XX
 XX Mus musculus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note="signal peptide"
 FT Protein 20..137
 FT /note="mature protein; this sequence given as sequence
 FT number 45 in the specification"
 XX
 PN WO200164249-A1.
 XX
 XX 07-SEP-2001.
 PD
 XX
 XX 30-AUG-2000; 2000WO-JP005886.
 PF
 XX
 XX 28-FEB-2000; 2000JP-00052414.
 PR
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Saito H, Tsunenari T, Onuma E, Sato K;
 PI
 XX
 DR MPI: 2001-550131/61.
 DR N-PSDB; AAH75106..
 XX
 XX Tissue decomposition inhibitor that prevents parathyroid hormone
 PT associated proteins from binding to its receptor.
 PT
 XX
 XX Example 1; Page 106; 132pp; Japanese.
 XX
 XX The specification describes a tissue decomposition inhibitor, which
 CC comprises a substance that inhibits peptides associated with parathyroid
 CC hormone (PTH) from binding with their receptor. The method is used to
 CC inhibit tissue decomposition caused by cancer cachexia, septicemia, heavy
 CC external injury or muscular dystrophy, and for treating patients with
 CC elevated cytokine (interleukin-6, granulocyte colony stimulating factor,
 CC interleukin-11 and leukemia inhibitory factor) levels. It may also be
 CC used for preventing weight loss caused by cancer cachexia. The present
 CC sequence represents a murine antibody fragment which is directed against
 CC PTH
 CC
 CC
 SQ Sequence 137 AA;

Query Match 81.7%; Score 559; DB 4; Length 137;
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVAVVSSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60
 DB 1 MNFGSLIFLVVLKGVQCEVAVVSSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60
 QY 61 DKRLMVAVATISSGGSTFYADVVKGRFTISRANAKNTLYLQMSLKSEDTALYYCARDDL 120
 DB 61 DKRLMVAVATISSGGSTFYADVVKGRFTISRANAKNTLYLQMSLKSEDTALYYCARDDL 120
 QY 121 FN---WGQGTLLTVSS 133
 DB 121 MTFYFVWGQGTLLTVSA 137

RESULT 13
 ID AAG64775
 AC AAG64775 standard; protein; 137 AA.
 XX
 XX AAG64775;
 DT 08-OCT-2001 (first entry)
 DE Mouse anti-PTHrP mAb 23-57-137-1 VH precursor.
 XX
 XX Parathyroid hormone-related peptide; PTHrP; antagonist;

KW calcium regulation disorder; serum calcium concentration; VH;
 KW humoral hypercalcaemia of malignancy; cytostatic; analgesic; mouse;
 KW murine; monoclonal antibody 23-57-137-1; heavy chain variable region.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= signal_peptide
 FT 20..137
 FT Protein /note= "Mature VH"

PN W0200147554-A1.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000MO-JP009339.

XX 28-DEC-1999; 99JP-00375203.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Yamazaki T, Hayaoka A, Koga A;

DR WPI; 2001-425590/45.

DR N-PSDB; AAH76644.

XX Composition for treating diseases of calcium regulation and for use as an
 PT analgesic, comprises an antibody recognizing parathyroid hormone related
 PT peptide.

XX Disclosure; Page 103-104; 128pp; Japanese.

XX The invention relates to a stabilised composition of an antibody which
 CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.
 CC The composition consists of a solution of the antibody in a buffer of pH
 CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid
 CC and their salts. The composition has increased storage stability,
 CC especially at elevated temperatures. The composition antagonises the
 CC action of PTHrP, and may be used in the treatment of diseases involving
 CC disturbances of calcium regulation (high or low serum calcium
 CC concentration) such as humoral hypercalcaemia of malignancy and as an
 CC analgesic. The present sequence represents the heavy chain variable
 CC region (VH) precursor of anti-human PTHrP murine monoclonal antibody 23-
 CC 57-137-1

XX Sequence 137 AA;

XX Query Match

Best Local Similarity 81.7%; Score 559; DB 4; Length 137;
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVCEVKYVESGGGLVYPGASLKLSCAASGTFPSNYGMSWRQTS 60

DB 1 MNFGSLIFLVVLKGVCEVKYVESGGGLVYPGASLKLSCAASGTFPSNYGMSWRQTS 60

QY 61 DKRLIEWVASISGGDSFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120

DB 61 DKRLIEWVASISGGDSFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120

QY 121 FN---WGQGTLLTVSS 133

DB 121 MTFEAYWGGTLLTVSSA 137

Db 121 MTFEAYWGGTLLTVSSA 137

RESULT 14
 AAG63393
 ID AAG63393 standard; protein; 137 AA.

XX AAG63393;

XX 15-OCT-2001 (first entry)

XX

DE Amino acid sequence of a murine polypeptide.

XX Parathyroid hormone-associated peptide; PTHrP; dental disease.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..137
 FT /note= "mature protein"

PN W0200154725-A1.

XX 02-AUG-2001.

XX 14-DEC-2000; 2000MO-JP008875.

XX 25-JAN-2000; 2000JP-00083034.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Kato A, Suzuki M, Sugimoto T;

DR WPI; 2001-465459/50.

DR N-PSDB; AAH74284.

XX Parathyroid hormone-associated peptide binding inhibitors useful for
 PT treating dental disease.

XX Disclosure; Page 111-112; 140pp; Japanese.

XX The specification describes a treatment for dental diseases. The
 CC treatment comprises a substance that inhibits binding between parathyroid
 CC hormone-associated peptide and its receptor. The present sequence
 CC represents a murine protein, which is used in the course of the invention

XX Sequence 137 AA;

XX Query Match

Best Local Similarity 81.7%; Score 559; DB 4; Length 137;
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVCEVKYVESGGGLVYPGASLKLSCAASGTFPSNYGMSWRQTS 60

DB 1 MNFGSLIFLVVLKGVCEVKYVESGGGLVYPGASLKLSCAASGTFPSNYGMSWRQTS 60

QY 61 DKRLIEWVASISGGDSFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120

DB 61 DKRLIEWVASISGGDSFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120

QY 121 FN---WGQGTLLTVSS 133

DB 121 MTFEAYWGGTLLTVSSA 137

Db 121 MTFEAYWGGTLLTVSSA 137

RESULT 15
 ABB95208
 ID ABB95208 standard; protein; 137 AA.

XX ABB95208;

XX 17-JUN-2002 (first entry)

XX Mouse joint disease related protein SEQ ID NO 57.

XX Joint disease; PTH; PTHrP; parathyroid hormone-related peptide;
 KW parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.

XX Mus musculus.

XX W0200213865-A1.

XX 21-FEB-2002.

XX

PF 15-AUG-2001; 2001WO-JP007044.

PR 16-AUG-2000; 2000JP-00247013.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Yoshikawa H;

DR WPI; 2002-257551/30.

DR N-PSDB; ABL94765.

PT Agents for ameliorating symptoms caused by joint diseases relating to PTH
PT or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors on
PT receptor binding of parathyroid hormone-related peptide.

PS Disclosure; Page 88-89; 112pp; Japanese.

The invention relates to agents for ameliorating symptoms causing joint diseases, containing a substance inhibiting the binding of a parathyroid hormone-related peptide to its receptor as active ingredient. The agents have osteopathic activity are useful for ameliorating symptoms caused by joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis and arthritis deformans. The agents particularly improve the lowering of bone amount or suppression of bone reduction. The present sequence is that of a joint disease related protein, useful to the invention

SQ Sequence 137 AA;

Query Match 81.7%; Score 559; DB 5; Length 137;

Matches 107; Conservative 13; Mismatches 13

Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGLSLFLVLVLKGVQCEVKVESGGGLVKPGASLKLSCAASGFTFSNYGMSWRQTS 600

Db 1 M N F G L S L F L A L I L K G V Q C E V Q L V E S G G D L V K P G G S L K L S C A S G F T F S S Y G M S W I R Q T P 600

61 DKLEWVASISSGSDSTFYADNVKGRFTISR ENAKNTLYLQMSSLSKSED TALYYCARDL 120

Db 61 DKRLWVATISSGGSYYYPDSVKGRFTISRDNKNTLYLQMSLSKSEDAMFYCARQT 120

QY 121 FN---WGQGTTLTVSS 133

Db 121 MTFAYWGQGLTVSA 137

Search completed: May 25, 2005, 15:47:16
Job time : 62.6028 secs

Job time : 62.6028 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: May 25, 2005, 15:37:02 ; Search time 16.5786 Seconds
(without alignments)
598.864 Million cell updates/sec

Title: US-10-006-773A-9
Perfect score: 684
Sequence: 1 MNFGSLIFLVVLKGVQCE.....YCARDLFFMGCGTTLTVSS 133

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	81.7	135	3	US-08-579-378A-16
2	545.5	79.8	138	2	US-08-379-057-14
3	544.5	79.6	136	3	US-08-976-183A-33
4	543.5	79.5	136	3	US-08-976-183A-31
5	540.5	79.0	136	3	US-08-976-183A-32
6	539.5	78.9	136	3	US-08-976-183A-34
7	538.5	78.7	136	1	US-08-253-877C-57
8	538.5	78.7	136	1	US-08-452-164A-57
9	534.5	78.1	247	5	PCT-US94-07659-2
10	532.5	77.9	140	3	US-08-836-561-23
11	532.5	77.9	140	4	US-09-434-122-23
12	529	77.3	135	3	US-08-579-378A-20
13	527.5	77.1	158	2	US-08-653-402B-6
14	522.5	76.4	138	1	US-08-053-171-7
15	522.5	76.4	138	1	US-08-053-171-11
16	515	75.3	139	1	US-08-129-930B-96
17	515	75.3	139	3	US-08-134-346A-51
18	515	75.3	139	3	US-08-976-288A-96
19	511.5	74.8	158	2	US-08-653-402B-10
20	499	73.0	159	2	US-08-653-402B-2
21	498	72.8	255	2	US-07-690-192-4
22	496.5	72.6	170	2	US-08-652-558-40
23	495	72.4	135	5	PCT-US95-07302-8
24	487	71.2	135	3	US-08-619-491-8
25	486.5	71.1	130	4	US-09-225-322B-8
26	486.5	71.1	130	4	US-09-764-304-8
27	484.5	70.8	130	4	US-09-225-322B-18

28	484.5	70.8	130	4	US-09-764-304-18	Sequence 18, Appl
29	483	70.6	135	3	US-08-619-491-4	Sequence 4, Appl1
30	483	70.6	135	5	PCT-US95-07302-4	Sequence 4, Appl1
31	482.5	70.5	121	1	US-08-339-582-2	Sequence 2, Appl1
32	480	70.2	131	1	US-08-259-372A-4	Sequence 4, Appl1
33	480	70.2	131	1	US-08-468-671-4	Sequence 4, Appl1
34	474	69.3	144	1	US-08-026-320A-2	Sequence 2, Appl1
35	474	69.3	463	4	US-09-472-087-64	Sequence 4, Appl1
36	474	69.3	463	4	US-09-472-087-68	Sequence 68, Appl
37	473.5	69.2	470	4	US-09-859-053-32	Sequence 32, Appl
38	471.5	68.9	470	4	US-09-859-053-36	Sequence 36, Appl
39	471	68.9	463	4	US-09-472-087-1	Sequence 1, Appl1
40	471	68.9	463	4	US-09-472-087-63	Sequence 63, Appl
41	471	68.9	463	4	US-09-472-087-64	Sequence 64, Appl
42	470.5	68.8	217	5	PCT-US94-14106-59	Sequence 59, Appl
43	470.5	68.8	464	4	US-09-472-087-2	Sequence 2, Appl1
44	470.5	68.8	464	4	US-09-472-087-66	Sequence 66, Appl
45	470	68.7	141	1	US-08-259-372A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-579-378A-16

Query Match	81.7%;	Score 559;	DB 3;	Length 135;
Best Local Similarity	82.4%;	Pred. No. 4.8e-53;		
Matches 112;	Conservative 11;	Mismatches 9;	Indels 4;	Gaps 3;

[illegible]

```
QY      61 DKRLIEWASISSGGDSTFYADNVKGRFTISSENAKNTLYLQWSSLKEDTALYYCAR--D 118
      :|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EKRLIEWASISTGG-STYYPDPSVKGRFTISDNARNILYLQWSSLRSDTAMYYCARDYD 119
```

Qy	119	DLFN-WGQGTTLTVSS	133
		:	
Db	120	GYFDYWGQGTTLTVSS	135

RESULT 2

US-08-379-057-14
; Sequence 14, Application US/08379057
; Patent No. 5876950

```

1 GENERAL INFORMATION:
2 APPLICANT: Siadek, Anthony W.
3 APPLICANT: Hollenbaugh, Diane L.
4 APPLICANT: Gilliland, Lisa K.
5 APPLICANT: Gordon, Marcia L.
6 APPLICANT: Bajorath, Jurgen
7 APPLICANT: Aruffo, Alejandro A.
8 TITLE OF INVENTION: Monoclonal Antibodies Specific For
9 TITLE OF INVENTION: Different Epitopes of Human gp13 and Methods For Their Use
10 TITLE OF INVENTION: In Diagnosis and Therapy
11 NUMBER OF SEQUENCES: 57

```

FRAGMENT TYPE: N-terminal
US-08-379-057-14

```

Query Match      79.8%; Score 545.5; DB 2; Length 138;
Best Local Similarity 77.0%; Pred. No. 1.4e-51;
Matches 107; Conservative 14; Mismatches 11; Indels 7; Gaps
Qy      1 MNRGLSLIFLVYIKGVQCEVKVQVESGGGLVPRGASIKLSCAASGFTFSNYGMSWYRQTS 60
Db      1 MNRGFSLSIFLVYIKGVQCEVKLVESGGGLVPRGASIKLSCCTTSGFTFNMYASWYRQTP 60

```

[illegible]

RESULT 3
US-08-976-183A-33
; Sequence 33, Application US/08976183A

RESULT 3

US-08-976-183A-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026

? GENERAL INFORMATION: ?
 ? APPLICANT: King, David J. ?
 ? APPLICANT: Adair, John R. ?
 ? APPLICANT: Owens, Raymond J. ?
 ? TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33 ?
 ? TITLE OF INVENTION: ANTIGEN ?
 ? NUMBER OF SEQUENCES: 55 ?
 ? CORRESPONDENCE ADDRESS: ?
 ? ADDRESSEE: FOLEY & LARDNER ?

Query Match	79.6%	Score 544.5	DB 3	Length 136
Best Local Similarity	77.9%	Pred. No. 1.8e-51		
Matches 106, Conservative	13	Mismatches 14	Indels 3	Gaps 1

QY 1 MNEGLSLILVLYLVKGVQCEVAVVBSGGGLYKPGASLKLCSAAGSGPFFSNYGMSSWRQTS 60

Db 1 MNEGLSLILVLYLVKGVQCEVAVVBSGGGLYKPGASLKLCSAAGSGPFFSNYGMSSWRQTP 60

QY 61 DKLELVVASISSGGSTFYADNVKRPFIISSENAKNLYLYLQMSLLKSEDTNALLYCARDLL 120

```

61 DKLEWVASISSGGSTFYADNVKRFITSRNAKNTLYLOMSLSKSEDTALYYCARDDL 120
:|||||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:

```

Db 61 EKRLEWVATISSGGSTYTLVDSVKGRFTISRDSARNTLYLQWSSLRSEDTALYYCAPTTV 120
QY 121 F---NMGGGTLTVSS 133
Db 121 VPFAYWGQGLTVTVA 136

RESULT 4
US-08-976-183A-31
Sequence 31, Application US/08976183A
Patent No. 6307026
GENERAL INFORMATION:
APPLICANT: King, David J.
APPLICANT: Adair, John R.
APPLICANT: Owens, Raymond J.
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,183A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595,848
FILING DATE: 02-FEB-1996
APPLICATION NUMBER: PCT/GB93/02529
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-183A-31

Query Match 79.5%; Score 543.5; DB 3; Length 136;
Best Local Similarity 77.2%; Pred. No. 2.3e-51;
Matches 105; Conservative 14; Mismatches 14; Indels 3; Gaps 1;
QY 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASLKLSKSCAASGFTSNYGMWVRQTS 60
Db 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASLKLSKSCAASGFTSNYGMWVRQTS 60
QY 61 DKRLWVASISSGGSTFYADNVKGRFTISRDNANTLYLQWSSLRSEDTALYYCAPDDL 120
Db 61 EKRLEWVATISSGGSTYTLVDSVKGRFTISRDSARNTLYLQWSSLRSEDTALYYCAPTTV 120
QY 121 F---NMGGGTLTVSS 133

Db 121 VPFAYWGQGLTVTVA 136

RESULT 5
US-08-976-183A-32
Sequence 32, Application US/08976183A
Patent No. 6307026
GENERAL INFORMATION:
APPLICANT: King, David J.
APPLICANT: Adair, John R.
APPLICANT: Owens, Raymond J.
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,183A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595,848
FILING DATE: 02-FEB-1996
APPLICATION NUMBER: PCT/GB93/02529
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-183A-32

Query Match 79.0%; Score 540.5; DB 3; Length 136;
Best Local Similarity 77.2%; Pred. No. 4.9e-51;
Matches 105; Conservative 13; Mismatches 15; Indels 3; Gaps 1;
QY 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASLKLSKSCAASGFTSNYGMWVRQTS 60
Db 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASLKLSKSCAASGFTSNYGMWVRQTS 60
QY 61 DKRLWVASISSGGSTFYADNVKGRFTISRDNANTLYLQWSSLRSEDTALYYCAPDDL 120
Db 61 EKRLEWVATISSGGSTYTLVDSVKGRFTISRDSARNTLYLQWSSLRSEDTALYYCAPTTV 120
QY 121 F---NMGGGTLTVSS 133
Db 121 VPFAYWGQGLTVTVA 136

RESULT 6
US-08-976-183A-34
; Sequence 34, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5339
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-34
Query Match 78.9%; Score 539.5; DB 3; Length 136;
Best Local Similarity 76.5%; Pred. No. 6,3e-51;
Matches 104; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hamann, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Halleck, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3326
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57
Query Match 78.7%; Score 538.5; DB 1; Length 136;
Best Local Similarity 76.5%; Pred. No. 8,1e-51;
Matches 104; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

TITLE OF INVENTION: Conjugates of Methylcrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-57

Query Match 78.7%; Score 538.5; DB 2; Length 136;
Best Local Similarity 76.5%; Pred. No. 8.1e-51;
Matches 104; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGSLFLVLVLTGKVCCEKVGKGGGLYKPGASLKLSCAASGFTSNYGMVNRQTS 60
DB 1 MNFGSLFLVLVLTGKVCCEKVGKGGGLYKPGASLKLSCAASGFTSNYGMVNRQTS 60
QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSDTLALYCARDL 120
DB 61 EKRLWVAIVSSGGSYTYLDSVKGRFTISRBNKNTLYLQMSLSKSDTLALYCARPTV 120
QY 121 F---NMGGTTLTVSS 133
DB 121 VPPAVWGQTLTVSSA 136

RESULT 9
PCT-US94-07659-2
Sequence 2, Application PC/TUS9407659
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corp.
ADDRESS: Intellectual Property
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Suton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 78.1%; Score 534.5; DB 5; Length 247;
Best Local Similarity 76.8%; Pred. No. 4.7e-50;
Matches 106; Conservative 12; Mismatches 15; Indels 5; Gaps 2;

QY 1 MNFGSLFLVLVLTGKVCCEKVGKGGGLYKPGASLKLSCAASGFTSNYGMVNRQTS 60
DB 1 MNFGSLFLVLVLTGKVCCEKVGKGGGLYKPGASLKLSCAASGFTSNYGMVNRQTS 60
QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSDTLALYCARDL 120
DB 61 EKRLWVAIVSSGGGTYPTVVKGRFTISRBNKNTLYLQMSLSKSDTLALYCARGV 120
QY 121 ---FN-WGGTTLTVSS 133
DB 121 RRGYFDVWGAGTTLTVSS 138

RESULT 10
US-08-836-561-23
Sequence 23, Application US/08836561
Patent No. 6018032
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: IIDA, Akihito
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
TITLE OF INVENTION: Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561

FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, IIT, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-836-561-23

Query Match 77.9%; Score 532.5; DB 3; Length 140;
Best Local Similarity 72.1%; Pred. No. 3.8e-50;
Matches 101; Conservative 17; Mismatches 15; Indels 7; Gaps 1;

QY 1 MNFGSLIFLVILKGVQCEVKVSGGLVKGASLKISCAASGFTFSNYGMSWVRQTS 60
DB 1 MNFGSLIFLVILKGVQCEVKVSGGLVKGASLKISCAASGFTFSNYGMSWVRQTS 60
QY 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNAKOTLYLQMSLSKSEPTALYYCARDLU 120
DB 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNAKOTLYLQMSLSKSEPTALYYCARDLU 120
QY 121 FN-----WGQTTTLTVSS 133
DB 121 YGNRYAMDYWGQTSVTSS 140

RESULT 11
US-09-434-122-23
Sequence 23, Application US/09434122
Patent No. 6538111
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihito
ANAZAWA, Hideharu
HANAI, No. 6538111uo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,122
FILING DATE: 05-NO. 6538111-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, IIT, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-434-122-23

Query Match 77.9%; Score 532.5; DB 4; Length 140;
Best Local Similarity 72.1%; Pred. No. 3.8e-50;
Matches 101; Conservative 17; Mismatches 15; Indels 7; Gaps 1;

QY 1 MNFGSLIFLVILKGVQCEVKVSGGLVKGASLKISCAASGFTFSNYGMSWVRQTS 60
DB 1 MNFGSLIFLVILKGVQCEVKVSGGLVKGASLKISCAASGFTFSNYGMSWVRQTS 60
QY 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNAKOTLYLQMSLSKSEPTALYYCARDLU 120
DB 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNAKOTLYLQMSLSKSEPTALYYCARDLU 120
QY 121 FN-----WGQTTTLTVSS 133
DB 121 YGNRYAMDYWGQTSVTSS 140

RESULT 12
US-08-579-378A-20
Sequence 20, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,005
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-578-20

Query Match 77.3%; Score 529; DB 3; Length 135;
Best Local Similarity 77.9%; Pred. No. 8.7e-50;
Matches 106; Conservative 14; Mismatches 12; Indels 4; Gaps 3;

QY 1 MNFGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
DB 1 MNFGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 118
DB 61 GKGLEWVASISITGG-STYIPDSVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 119
QY 119 DLFN-WGQGTTLTVSS 133
DB 120 GFVDYWGQGTTLTVSS 135

RESULT 13
US-08-653-402B-6
Sequence 6, Application US/08653402B
Patent No. 5969107
GENERAL INFORMATION:
APPLICANT: CARCELLER, Ana
APPLICANT: ROSELL, Elisabet
APPLICANT: GOMEZ, Alicia
APPLICANT: ADEN, Jaume
APPLICANT: PUIGATS, Jaume
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Miller, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,402B
FILING DATE: 24-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95107967.2
FILING DATE: 26-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: MERCK 1781
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-653-402B-6

Query Match 77.1%; Score 527.5; DB 2; Length 158;
Best Local Similarity 74.3%; Pred. No. 1.5e-49;
Matches 107; Conservative 12; Mismatches 14; Indels 11; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
DB 1 MDGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 118
DB 61 EKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 120
QY 119 -----DLFNWGQGTTLTVSS 133
DB 121 RDSSGYVGYAIDYWGQGTSTVSS 144

RESULT 14
US-08-053-171-7
Sequence 7, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-053-171-7

Query Match 76.4%; Score 522.5; DB 1; Length 138;
Best Local Similarity 74.6%; Pred. No. 4.5e-49;
Matches 103; Conservative 14; Mismatches 16; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
DB 1 MNFGSLIFLVYLVKGVQCEVYVESGGGLVYKPGASLKSCAASGFTFSNYGMSWVROT 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 120

```
Db      61 EKRLWVAIISNGSGSHYDSVKGRTISRDNKNTLYLQMSRLRSEDTAMTHCARGMD 120
QY      121 FN-----WGQGTTLTVSS 133
      :      :      :      :      :      :      :      :      :      :
Db      121 YGAMFAYWGQGTTLTVTSA 138

RESULT 15
US-08-053-171-11
; Sequence 11, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-171-11

Query Match      76.4%; Score 522.5; DB 1; Length 138;
Best Local Similarity 74.6%; Pred. No. 4.5e-49;
Matches 103; Conservative 14; Mismatches 16; Indels 5; Gaps 1;

QY      1 MNFGSLIFLVLYLKGVQCEVKVVGSGGLVKPQASIKLSGASGFTPSNYGSMWVROT 60
      :      :      :      :      :      :      :      :      :      :
Db      1 MNGLSLIFLVLYLKGVQCEVKLVESGGGLVQPGSILKLSGATSGFTPSDYMYWVROT 60

QY      61 DKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSRLRSEDTALYYCARDL 120
      :      :      :      :      :      :      :      :      :      :
Db      61 EKRLWVAIISNGSGSHYDSVKGRTISRDNKNTLYLQMSRLRSEDTAMTHCARGMD 120

QY      121 FN-----WGQGTTLTVSS 133
      :      :      :      :      :      :      :      :      :      :
Db      121 YGAMFAYWGQGTTLTVTSA 138
```

Search completed: May 25, 2005, 15:58:23
Job time : 16.5786 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: May 25, 2005, 15:37:58 ; Search time 61.3656 Seconds
(without alignments)
724.991 Million cell updates/sec

Title: US-10-006-773a-9

Perfect score: 684
Sequence: 1 MNFGSLFLVLVLRGVQCE.....YCARDLFFMGQGITLVSS 133

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_A1:

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	100.0	133	US-10-006-773-9	Sequence 9, Appli
2	609.5	89.1	138	US-10-010-942B-4	Sequence 4, Appli
3	609.5	89.1	138	US-10-388-389-8	Sequence 4, Appli
4	609.5	89.1	138	US-10-703-713-8	Sequence 4, Appli
5	609.5	89.1	138	US-10-704-070-8	Sequence 4, Appli
6	609.5	89.1	138	US-10-232-030-4	Sequence 4, Appli
7	590	86.3	139	US-10-006-773-17	Sequence 17, Appli
8	569.5	83.3	146	US-10-281-479A-23	Sequence 23, Appli
9	569.5	83.3	146	US-10-286-132A-23	Sequence 23, Appli
10	569.5	83.3	146	US-10-275-180A-23	Sequence 23, Appli
11	559.5	81.8	144	US-09-881-823-12	Sequence 12, Appli
12	559	81.7	137	US-09-423-800-76	Sequence 76, Appli
13	559	81.7	137	US-10-337-981-76	Sequence 76, Appli

14	550.5	80.5	138	US-10-010-942B-8	Sequence 8, Appli
15	550.5	80.5	138	US-10-388-389-8	Sequence 8, Appli
16	550.5	80.5	138	US-10-703-713-8	Sequence 8, Appli
17	550.5	80.5	138	US-10-704-070-8	Sequence 8, Appli
18	550.5	80.5	138	US-10-232-030-8	Sequence 8, Appli
19	550.5	80.5	140	US-10-006-773-4	Sequence 4, Appli
20	549.5	80.3	146	US-10-476-265-20	Sequence 20, Appli
21	548.5	80.2	138	US-10-010-942B-12	Sequence 12, Appli
22	548.5	80.2	138	US-10-388-389-12	Sequence 12, Appli
23	548.5	80.2	138	US-10-703-713-12	Sequence 12, Appli
24	548.5	80.2	138	US-10-704-070-12	Sequence 12, Appli
25	548.5	80.2	138	US-10-232-030-12	Sequence 12, Appli
26	536.5	78.4	140	US-09-286-240-4	Sequence 4, Appli
27	532.5	77.9	140	US-10-283-349-23	Sequence 23, Appli
28	526.5	77.0	158	US-10-226-795-32	Sequence 32, Appli
29	516.5	75.5	143	US-10-469-104-17	Sequence 17, Appli
30	515	75.3	139	US-09-947-839-96	Sequence 96, Appli
31	510.5	74.6	140	US-10-365-123-51	Sequence 51, Appli
32	509	74.4	137	US-09-423-800-77	Sequence 77, Appli
33	509	74.4	137	US-10-337-981-77	Sequence 77, Appli
34	507.5	74.2	146	US-10-401-344-2	Sequence 2, Appli
35	506	74.0	143	US-09-791-551-117	Sequence 117, App
36	506	74.0	177	US-10-633-629-64	Sequence 64, Appli
37	504.5	73.8	159	US-10-291-265-333	Sequence 333, App
38	503.5	73.5	138	US-10-038-591-46	Sequence 46, Appli
39	502.5	73.5	138	US-09-796-744-15	Sequence 15, Appli
40	502.5	73.5	138	US-10-231-452-62	Sequence 62, Appli
41	502.5	73.5	146	US-10-938-353-70	Sequence 70, Appli
42	502.5	73.5	474	US-09-848-832-3	Sequence 3, Appli
43	502.5	73.5	474	US-10-225-108A-3	Sequence 3, Appli
44	502.5	73.5	474	US-10-461-148-1	Sequence 1, Appli
45	502	73.4	461	US-10-938-353-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-10-006-773-9
; Sequence 9, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti.
; FILE REFERENCE: 003
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-9

Query Match 100.0%; Score 684; DB 13; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.6e-57;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNFGSLFLVLVLRGVQCEVKVVGSGGLKPKGASIKLSCAASGFTFSNMGSMVNRQTS	60
DB	1	MNFGSLFLVLVLRGVQCEVKVVGSGGLKPKGASIKLSCAASGFTFSNMGSMVNRQTS	60
QY	61	DKRLWVASISSGGSTFYADNVKGRFTISRENNKNTLYLQMSLSKSDTALYYCARDL	120
DB	61	DKRLWVASISSGGSTFYADNVKGRFTISRENNKNTLYLQMSLSKSDTALYYCARDL	120
QY	121	FNMGQGITLVSS 133	
DB	121	FNMGQGITLVSS 133	

```
RESULT 2
US-10-010-942B-4
; Sequence 4, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4
```

```
Query Match      89.1%; Score 609.5; DB 14; Length 138;
Best Local Similarity 87.0%; Pred. No. 8.5e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;
```

```
QY      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQTS 60
         |||||
DB      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQNS 60
         |||||
QY      61 DKRLWVASISGGGDTFYADVVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
DB      61 DKRLWVASIRSGGRTYSDNVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
QY      121 FN-----WGQGTTLTVSS 133
         ::|||
DB      121 YGSSSDYWGQGTTLTVSS 138
         |||||
```

```
RESULT 3
US-10-388-389-4
; Sequence 4, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-4
```

```
Query Match      89.1%; Score 609.5; DB 15; Length 138;
```

```
Best Local Similarity 87.0%; Pred. No. 8.5e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;
```

```
QY      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQTS 60
         |||||
DB      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQNS 60
         |||||
QY      61 DKRLWVASISGGGDTFYADVVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
DB      61 DKRLWVASIRSGGRTYSDNVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
QY      121 FN-----WGQGTTLTVSS 133
         ::|||
DB      121 YGSSSDYWGQGTTLTVSS 138
         |||||
```

```
RESULT 4
US-10-703-713-4
; Sequence 4, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-4
```

```
Query Match      89.1%; Score 609.5; DB 16; Length 138;
Best Local Similarity 87.0%; Pred. No. 8.5e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;
```

```
QY      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQTS 60
         |||||
DB      1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVPGASLKLSCAASGFTFSNYGMSWVRQNS 60
         |||||
QY      61 DKRLWVASISGGGDTFYADVVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
DB      61 DKRLWVASIRSGGRTYSDNVKGRFTISRANAKTLYLQMSLSKSEDTALYYCVRDYL 120
         |||||
QY      121 FN-----WGQGTTLTVSS 133
         ::|||
DB      121 YGSSSDYWGQGTTLTVSS 138
         |||||
```

```
RESULT 5
US-10-704-070-4
; Sequence 4, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
US-10-704-070-4
```

FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/704,070
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 138
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-704-070-4

Query Match 89.1%; Score 609.5; DB 16; Length 138;
Best Local Similarity 87.0%; Pred. No. 8,5e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQTS 60
DB 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQNS 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANAKNTLYLQWSSLKSEDTALYYCARDL 120
DB 61 DKRLWVASISGGRTYSDNVKGRFTISRANAKNTLYLQWSSLKSEDTALYYCVRDH 120
QY 121 FN-----WGCGTTLTVSS 133
DB 121 YGSSSDYWGQGTTLTVSS 138

RESULT 6
US-10-232-030-4
Sequence 4, Application US/10232030
Publication No. US20050009150A1
GENERAL INFORMATION:
APPLICANT: Dale Schenk
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002CN
CURRENT APPLICATION NUMBER: US/10/232,030
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR FILING DATE: 1998-11-30
PRIOR APPLICATION NUMBER: US 09/723,713
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/322,289
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 138
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-232-030-4

Query Match 89.1%; Score 609.5; DB 17; Length 138;
Best Local Similarity 87.0%; Pred. No. 8,5e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQTS 60
DB 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQNS 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANAKNTLYLQWSSLKSEDTALYYCARDL 120
DB 61 DKRLWVASISGGRTYSDNVKGRFTISRANAKNTLYLQWSSLKSEDTALYYCVRDH 120
QY 121 FN-----WGCGTTLTVSS 133
DB 121 YGSSSDYWGQGTTLTVSS 138

RESULT 7
US-10-006-773-17
Sequence 17, Application US/10006773
Publication No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
FILE REFERENCE: 003
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 139
TYPE: PRT
ORGANISM: Mus sp.
US-10-006-773-17

Query Match 86.3%; Score 590; DB 13; Length 139;
Best Local Similarity 83.5%; Pred. No. 6e-48;
Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQTS 60
DB 1 MNFGSLFLVYLKGVCEVNVESGGGLVYPGASLKLSCAASGFTSNYGMWVRQNS 60
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANAKNTLYLQWSSLKSEDTALYYCARDL 119
DB 61 DKRLWVASISGTGANTYPPDNVGRFTISRANAKNTLYLQWSSLKSEDTALYYCARDH 120
QY 120 -----LFNWGGTTLTVSS 133
DB 121 SVGCWPAFWGQGTTLTVSA 139

RESULT 8
US-10-281-479A-23
Sequence 23, Application US/10281479A
Publication No. US20030133932A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
APPLICANT: Lobuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
FILE REFERENCE: 21085,0029U6
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US2003013932A1e = Synthe
US-10-281-479A-23

Query Match 83.3%; Score 569.5; DB 14; Length 462;
Best Local Similarity 81.9%; Pred. No. 1,9e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 1 MNFGSLIFLVYLVKGVQCEVKVYSGGGIVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60
DB 1 MNFGSLIFLVYLVKGVQCEVMVLESGGIVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
QY 61 DKLEWVASISGGSDSTFPADVNGKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR--D 118
DB 61 EKRLWVATISSGGSYTYPPDSYKGRFTISRBNKNTLYLQMSLSKSEDTAMYYCARRGD 120
QY 119 DLFN--WGCGTTLTVSS 133
DB 121 SMITTDYWGCGTTLTVSS 138

RESULT 9
US-10-286-132A-23
Sequence 23, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Lobuglio, Albert S.
APPLICANT: Buchbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002917
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-23

Query Match 83.3%; Score 569.5; DB 14; Length 462;
Best Local Similarity 81.9%; Pred. No. 1,9e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;
QY 1 MNFGSLIFLVYLVKGVQCEVKVYSGGGIVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60
DB 1 MNFGSLIFLVYLVKGVQCEVMVLESGGIVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
QY 61 DKLEWVASISGGSDSTFPADVNGKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR--D 118
DB 61 EKRLWVATISSGGSYTYPPDSYKGRFTISRBNKNTLYLQMSLSKSEDTAMYYCARRGD 120

QY 119 DLFN--WGCGTTLTVSS 133
DB 121 SMITTDYWGCGTTLTVSS 138

RESULT 10
US-10-275-180A-23
Sequence 23, Application US/10275180A
Publication No. US20030190687A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTO-
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002905
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
US-10-275-180A-23

Query Match 83.3%; Score 569.5; DB 14; Length 464;
Best Local Similarity 81.9%; Pred. No. 2e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 1 MNFGSLIFLVYLVKGVQCEVKVYSGGGIVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60
DB 1 MNFGSLIFLVYLVKGVQCEVMVLESGGIVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
QY 61 DKLEWVASISGGSDSTFPADVNGKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR--D 118
DB 61 EKRLWVATISSGGSYTYPPDSYKGRFTISRBNKNTLYLQMSLSKSEDTAMYYCARRGD 120
QY 119 DLFN--WGCGTTLTVSS 133
DB 121 SMITTDYWGCGTTLTVSS 138

RESULT 11
US-09-881-823-12
Sequence 12, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 144
TYPE: PRT
ORGANISM: Murine
US-09-881-823-12

Query Match	81.8%	Score 559.5;	DB 9;	Length 144;
Best Local Similarity	76.1%;	Pred. No. 4.7e-45;		
Matches 108;	Conservative 15;	Mismatches 10;	Indels 9;	Gaps 1

[illegible]

```
Qy      61 DKRLRWVASISSGGDSTFYADNVKGFPTISRENAKNLTLYLQWSSLKSBDTALYYCARD-119
          :|||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 EKRLRWVASISSGTYTTYPDPSVKGFPTISRNAKNLTLYLQWSSLKSBDTAMYYCSRDDG-120
```

```
QY      120 -----LFNMGQGITLTVSS 133
          : |||||::|||
Db      121 SYGSYYYAMDYWGQGSTVTSS 142
```

RESULT 12
US-09-423-800-76
; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
JOURNAL INFORMATION

1 APPLICANT: TSUENHARI, TOSHIAKI
 2 APPLICANT: ISHII, KIMIE
 3 TITLE OF INVENTION: CACHEMIA REMEDY
 4 FILE REFERENCE: 04853-0036
 5 CURRENT APPLICATION NUMBER: US/09/423,800
 6 PRIORITY FILING DATE: 1999-11-12
 7 PRIOR APPLICATION NUMBER: PCT/JP98/02116
 8 PRIOR FILING DATE: 1998-05-13
 9 PRIOR APPLICATION NUMBER: JP 125505/1997
 10 PRIOR FILING DATE: 1997-05-15
 11 PRIOR APPLICATION NUMBER: JP 194445/1997
 12 PRIOR FILING DATE: 1997-07-18
 13 NUMBER OF SEQ ID NOS: 87
 14 SOFTWARE: PatentIn Ver. 2.1
 15 SEQ ID NO 76

Query Match	81.7%	Score 559	DB 9	Length 137
Best Local Similarity	78.1%	Pred. NO. 4.9e-45		
Matches 107; Conservative	13	Mismatches	13	Gaps 4
				Gaps 1

```

QY 1 MNGSLILFVLVLKVOCEVYKVSGGGLYVRGASLKLSCASGFTFSNNGMWKROT 60
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 MNGSLILFVLVLKVOCEVQVMSGGGLYVRGSLKLSCASGFTFSNGMSWIKOT 60
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 61 DKLELVASISSGGDSTFYADNVKGRFTISRANAGTLYLQMSLSKEDTALYCCARD 120
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 61 DKLELVATISSGGSTTYTPDSYKGRFTISRANAGTLYLQMSLSKEDTAMFYCAR 120
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 121 FN----WGQGTTLTVSS 133
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 121 MTFYALWGQGTTLTVTSA 137
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||

```

RESULT 13
US-10-337-981-76
Sequence 76, Application US/10337981
Publication No. US20030138424A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: TSUNENARI, TOSHIAKI
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/10/337, 981
CURRENT FILING DATE: 2003-01-08

```

; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-76

```

Query Match	81.7%;	Score 559;	DB 14;	length 137;
Best Local Similarity	78.1%;	Pred. No. 4.9e-45;		
Matches 107; Conservative	13;	Mismatches 13;	Indels 4;	Gaps 1

[illegible]

```

RESULT 14
US-10-010-942B-8
: Sequence 8, Application US/10010942B
: Publication No. US20030165496A1
: GENERAL INFORMATION:
: APPLICANT: Bas1, Gurig
: APPLICANT: Saldanha, Jose
: APPLICANT: Yednock, Ted
: TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
: TITLE OF INVENTION: BETA AMYLOID PEPTIDE
: FILE REFERENCE: ELN-002
: CURRENT APPLICATION NUMBER: US/10/010,942B
: CURRENT FILING DATE: 2002-12-06
: PRIOR APPLICATION NUMBER: US 60/251,892
: PRIOR FILING DATE: 2000-12-06
: NUMBER OF SEQ ID NOS: 63
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 138
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Humanized 3d6 heavy chain variable region
: NAME/KEY: SIGNAL
: LOCATION: (1)...(19)
US-10-010-942B-8

```

Query Match	80.5%;	Score 550.5;	DB 14;	Length 138;
Best Local Similarity	76.8%;	Pred. No. 3.2e-44;		
Matches 106; Conservative	15;	Mismatches 12;	Indels 5;	Gaps 1.

```

QY      1  MFMGSLILFLVYLVLKGVGCEVKNVSGGGVLKYPGASLILSCAAGGFFPSNYGMSWRQTS 60
DQ      1  MFMGSLILFLVYLVLKGVGCEVKNVSGGGVLKYPGASLILSCAAGGFFPSNYGMSWRQAP 60
QY      1  MFMGSLILFLVYLVLKGVGCEVKNVSGGGVLKYPGASLILSCAAGGFFPSNYGMSWRQAP 60
DQ      1  MFMGSLILFLVYLVLKGVGCEVKNVSGGGVLKYPGASLILSCAAGGFFPSNYGMSWRQAP 60
QY      61  DKRLKLEVASISSGGDSTPYADNVKGRFTISSENKANTLYLQMSLSKEDTALYYCARDL 120
DQ      61  GKLELWVASIRSGGRTYSDNVKGRFTISRDNKNSIYLQMSLRAEDTALYYCYRYDH 120
QY      121  FN-----WGQGTTLTVSS 133
DQ      121  FN-----WGQGTTLTVSS 133

```

Db 121 YSGSSDYWGQGLTVWSS 138

```
RESULT 15
US-10-388-389-8
; Sequence 8, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guritq
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: Eln-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3d6 heavy chain variable region
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-8
```

```
Query Match 80.5%; Score 550.5; DB 15; Length 138;
Best Local Similarity 76.8%; Pred. NO. 3.2e-44;
Matches 106; Conservative 15; Mismatches 12; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVKVESGGGLVKPGASIKLSCAAGFTFSNYGMSWVRQTS 60
Db 1 MNFGSLIFLVLVKGVQCEVGLLESGGGLVQPGGSLRUSCAAGFTFSNYGMSWVRQAP 60
QY 61 DKRLFNWASISGGGSTFTADNFKGRFTISRENAKNTLYIQMSLKSDEPTALYYCARDL 120
Db 61 GKLEFNWASIRSGGGRTYSDNFKGRFTISRDNAKNSLYIQMNSLRAPDPTALYYCVRYDH 120
QY 121 FN----WGQGLTVWSS 133
Db 121 YSGSSDYWGQGLTVWSS 138
```

Search completed: May 25, 2005, 16:06:51
Job time : 62.4906 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.8056 Seconds
(without alignments)
680.480 Million cell updates/sec

Title: US-10-006-773A-9

Perfect score: 684

Sequence: 1 MNFGSLIFLVLVKGVQCE.....YCARDDLFNMGQTTLVSS 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553.5	80.9	152	2 B26471	Ig heavy chain pre
2	552.5	80.8	138	2 S09258	Ig heavy chain V r
3	546	79.8	139	2 S38808	Ig heavy chain - m
4	517	75.6	117	1 HVM584	Ig heavy chain pre
5	515.5	75.4	142	2 C34903	Ig heavy chain pre
6	515	75.3	117	1 HVM534	Ig heavy chain pre
7	510	74.6	117	1 HVM539	Ig heavy chain pre
8	503.5	73.6	134	2 S31699	Ig heavy chain V r
9	502.5	73.5	140	2 S31588	Ig heavy chain V r
10	501.5	73.3	160	2 S05271	Ig heavy chain pre
11	498.5	72.9	138	2 S31666	Ig heavy chain V r
12	498	72.8	140	2 S70442	Ig heavy chain pre
13	493	72.1	117	1 HVM584	Ig heavy chain pre
14	491	71.8	117	1 HVM557	Ig heavy chain pre
15	490.5	71.7	140	2 S22657	Ig heavy chain pre
16	489	71.5	139	2 S31674	Ig heavy chain V r
17	488.5	71.4	140	2 S31686	Ig heavy chain V r
18	485.5	71.0	134	2 S31679	Ig heavy chain V r
19	483.5	70.7	139	2 I37781	Ig heavy chain V r
20	482	70.5	136	1 G1MS21	Ig heavy chain pre
21	481	70.3	136	2 S31587	Ig heavy chain V r
22	479.5	70.1	140	2 A30532	Ig heavy chain pre
23	476.5	69.7	136	2 S31615	Ig heavy chain pre
24	476	69.6	141	2 S31669	Ig heavy chain V r
25	475	69.4	137	2 S31701	Ig heavy chain V r
26	474	69.3	151	2 A60943	Ig heavy chain pre
27	472	69.0	147	2 I37780	Ig heavy chain pre
28	471.5	68.9	132	2 S31603	Ig heavy chain V r
29	470	68.7	117	2 A34964	Ig heavy chain pre

30	469	68.6	117	2 A45953	Ig heavy chain pre
31	469	68.6	119	2 F27888	Ig heavy chain V r
32	469	68.6	137	2 S78054	Ig heavy chain pre
33	468.5	68.5	130	2 P10098	Ig heavy chain pre
34	468.5	68.5	138	2 A30561	Ig heavy chain pre
35	466.5	68.2	135	2 E27888	Ig heavy chain V r
36	466.5	68.2	135	2 S31598	Ig heavy chain V r
37	466	68.1	254	2 B31790	Ig heavy chain V r
38	465	68.0	117	1 H3H26	Ig heavy chain pre
39	465	68.0	117	2 B34964	Ig heavy chain pre
40	465	68.0	118	2 PH0097	Ig heavy chain V r
41	464	67.8	135	2 I37778	Ig heavy chain V r
42	461	67.4	118	2 PH0096	Ig heavy chain V r
43	459.5	67.2	120	2 S55536	Ig heavy chain V r
44	459	67.1	121	2 I27887	Ig heavy chain V r
45	459	67.1	548	2 S38864	Ig epsilon chain C

ALIGNMENTS

```

RESULT 1
B26471
Ig heavy chain precursor V region (MAX33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: B26471; S70410
R:Buckel, P.; Hubner-Parafisz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A>Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: B26471
A:Molecule type: mRNA
A:Residues: 1-152 <BUC>
A:Cross-references: GB:M6163; NID:9195405; PIDN:AAA38292.1; PID:9195406
R:Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
A>Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
A:Reference number: S70410; MUID:91079775; PMID:2258702
A:Accession: S70410
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-19 <LEB>
A:Cross-references: EMBL:X53776; NID:952475; PIDN:CAA37792.1; PID:952476
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-152/Product: Ig heavy chain V region MAX33 #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      80.9%; Score 553.5; DB 2; Length 152;
Best Local Similarity 76.8%; Pred. No. 8.5e+42;
Matches 109; Conservative 11; Mismatches 13; Indels 9; Gaps 1;

QY      1 MNFGSLIFLVLVKGVQCEVYVSGGLVYRPGASLKLSCAASGFTSNGMSVNRQTS 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MNFGSLIFLVLVKGVQCEVGVSGGLVYRPGSLKLSCAASGFTSDVYMYWRQTP 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 DRLRPMVASISGGSTFYADNVKGRFTISRNANKTYLQWSLKSEDTALYCARDDL 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 ERLRPMVATISDGSYTYTPDSVKGRFTISRDNANKTYLQWSLKSEDTATYTCARDA 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      121 F-----NMVGQTTLVSS 133
        |||:|||||
DB      121 YGNYGDMADYWGQTSVTSS 142
        |||:|||||

RESULT 2
S09258
Ig heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)

```


C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: J0502
R/Ley, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A/Reference number: J0501; MUID:89279149; PMID:2499654
A/Accession: J0502
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-117 <LEV>
A/Cross-references: UNIPROT:P18526
A/Experimental source: strain BALB/cJ
A/Note: this sequence belongs to the VH7183 subfamily
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Diulfide bonds: #status predicted

Query Match 75.3%; Score 515; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 1.6e-38;
Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTS 60
Db 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTP 60
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117
Db 61 EKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117

RESULT 7

HVMS39
Ig heavy chain precursor V region (7-39) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: J0507
R/Ley, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A/Reference number: J0501; MUID:89279149; PMID:2499654
A/Accession: J0507
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-117 <LEV>
A/Cross-references: UNIPROT:P18530
A/Experimental source: strain BALB/cJ
A/Note: this sequence belongs to the VH7183 subfamily
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (7-39) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Diulfide bonds: #status predicted

Query Match 74.6%; Score 510; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 4.4e-38;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTS 60
Db 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTP 60
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117
Db 61 EKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117

RESULT 8
S31699
Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31699
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31699
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CU>
A/Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 503.5; DB 2; Length 134;
Best Local Similarity 71.6%; Pred. No. 1.9e-37;
Matches 96; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTS 60
Db 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROAP 60
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-DD 119
Db 61 GKLEWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-RD 120
Qy 120 LFNWGGFTLVVSS 133
Db 121 LDYWGCGTLVTVSS 134

RESULT 9

S31588
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31588
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31588
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <CU>
A/Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 502.5; DB 2; Length 140;
Best Local Similarity 68.6%; Pred. No. 2.4e-37;
Matches 96; Conservative 22; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROTS 60
Db 1 MNFGSLFLVYLKGVCEVAVESGGGLVPGASLKLSCAASGFTSNTGMSVWVROAP 60
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-D 119
Db 61 GKLEWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-KD 120
Qy 120 LFNWGGFTLVVSS 133
Db 121 YSNYTFDYWGCGTLVTVSS 140

RESULT 10
S05271
Ig heavy chain precursor - human (fragment)
C/Species: Homo sapiens (man)

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.8298 Seconds
(without alignments)
1050.544 Million cell updates/sec

Title: US-10-006-773a-9

Perfect score: 684

Sequence: 1 MNFGLSLIFLVVLKVGCE.....YCARDLLFVWGGTTLTVSS 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	82.9	487	2	Q99KA4 mus musculu
2	533.5	78.0	479	2	Q91WP5 mus musculu
3	527.5	77.1	486	2	Q91Z07 mus musculu
4	523	76.5	196	2	Q65ZL8 mus musculu
5	517	75.6	117	1	HV5A_MOUSE mus musculu
6	515	75.3	117	1	HV55_MOUSE mus musculu
7	510	74.6	117	1	HV59_MOUSE mus musculu
8	510	74.6	473	2	Q91Z05 mus musculu
9	502.5	73.5	480	2	Q91XEL mus musculu
10	494.5	72.3	485	2	Q6PDB8 mus musculu
11	492	72.1	117	1	HV53_MOUSE mus musculu
12	492	71.9	613	2	Q8WUK1 mus musculu
13	491	71.8	117	1	HV58_MOUSE mus musculu
14	488	71.3	606	2	Q6GMV2 mus musculu
15	487.5	71.3	597	2	Q96BB9 mus musculu
16	485.5	71.0	464	2	Q6WZU6 mus musculu
17	483.5	70.7	470	2	Q6PJ44 mus musculu
18	483.5	70.7	499	2	Q8NSK4 mus musculu
19	482	70.5	136	1	HV16_MOUSE mus musculu
20	480.5	70.2	478	2	Q6P1B1 mus musculu
21	480.5	70.2	493	2	Q6GMV2 mus musculu
22	474.5	69.4	119	2	Q920E7 mus musculu
23	470.5	68.8	255	2	Q6KBU5 mus musculu
24	470	68.7	573	2	Q8WU38 mus musculu
25	467.5	68.3	472	2	Q6N089 mus musculu
26	467	68.3	494	2	Q96K68 mus musculu
27	465	68.0	117	1	HV3C_HUMAN mus musculu
28	464	67.8	475	2	Q6WZU6 mus musculu
29	454	66.4	465	2	Q6P6C4 mus musculu
30	452	66.1	487	2	Q6ZVX0 mus musculu
31	450	65.8	544	2	Q6PJ95 mus musculu

32	449.5	65.7	493	2	Q8NCL6 mus musculu
33	449	65.6	479	2	Q6MZV6 mus musculu
34	448.5	65.6	466	2	Q61N78 mus musculu
35	447	65.4	475	2	Q6GMV7 mus musculu
36	446.5	65.3	466	2	Q6N096 mus musculu
37	445	65.1	473	2	Q6MZV7 mus musculu
38	439.5	64.3	470	2	Q7ZSW1 mus musculu
39	438.5	64.1	116	1	HV05_CARAU mus musculu
40	438.5	64.1	480	2	Q6N054 mus musculu
41	438	64.0	480	2	Q6MZV9 mus musculu
42	431.5	63.1	519	2	Q6N092 mus musculu
43	429.5	62.8	97	1	HV56_MOUSE mus musculu
44	427.5	62.5	487	2	Q80Z17 mus musculu
45	426.5	62.4	493	2	Q68CN4 mus musculu

ALIGNMENTS

RESULT 1
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefter C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Director MGC Project;
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AA004786.1; -.
DR HSSP; P01810; 2FBU.
DR MGI; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8B96DB333077B CRC64;

Query Match 82.9%; Score 567; DB 2; Length 487;
Best Local Similarity 78.3%; Pred. No. 4,7e-47;
Matches 112; Conservative 10; Mismatches 11; Indels 10; Gaps 2;

QY 1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60
1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60
DB 61 DKLEWVASISGGDSSTFYADNVKGRFTISRANKNTLYLQMSLSKSEPTALYYCARD 118
61 EKLEWVAITSSDGSSTYTYEDNVKGRFTISRANKNTLYLQMSLSKSEPTALYYCARD 120

QY 119 -----DLFN-WGCGTTLTSS 133
121 GSPYGGYRFDYWGCGTTITSS 143

RESULT 2
Q91WP5 PRELIMINARY; PRT; 479 AA.
ID Q91WP5;
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence update)
DE 1gh-V0558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RU Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAI13656.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS00835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 51603 MW; ECFBZD0877748584F CRC64;

Query Match 78.0%; Score 533.5; DB 2; Length 479;
Best Local Similarity 75.4%; Pred. No. 8.9e-44;
Matches 101; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60
1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60

DB 1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60
61 DKLEWVASISGGDSSTFYADNVKGRFTISRANKNTLYLQMSLSKSEPTALYYCARD 120
61 EKLEWVAITSSDGSSTYTYEDNVKGRFTISRANKNTLYLQMSLSKSEPTALYYCARD 120

QY 121 FN-WGCGTTLTSS 133
121 FVWAGAGTAVTSS 134

RESULT 3
Q91Z07 PRELIMINARY; PRT; 486 AA.
ID Q91Z07;
AC Q91Z07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence update)
DE 1gh-V0558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Director MGC Project;
RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAI10324.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS00835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

Query Match 77.1%; Score 527.5; DB 2; Length 486;
Best Local Similarity 71.3%; Pred. No. 3.5e-43;
Matches 102; Conservative 17; Mismatches 13; Indels 11; Gaps 2;

QY 1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60
1 MNFGLSLIFLVLTALKGVCCEVAVKGGGLVFKPGASLKLSCAASGFTFSNYGMSWROT 60

DB 61 DKLEWVASISGGDSSTFYADNVKGRFTISRANKNTLYLQMSLSKSEPTALYYCARD 120
61 ERLEWVAITSSG-STYYPDNVKGRTVSRDNKATLYLQMSLSKSEPTALYYCARD 119

Qy 121 -----FNMGGTTLTVSS 133
 Db 120 PIYYSGSYFDSMGCTITTVSS 142

RESULT 4

065ZL8 PRELIMINARY; PRT; 196 AA.
 AC 065ZL8; 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DN VHT183-DSP2-JH3-CH1 protein (Fragment).
 GN Name=VHT183-DSP2-JH3-CH1;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95362300; PubMed=7635518;
 RA Komori T., Sugiyama H.;
 RT "An aberrant splicing using a 3' cryptic splice site within the CH1
 exon induces truncated mu-chain production.";
 RL Immunology 85:166-170(1995).
 DR EMBL; S79401; AAB35023.2; -;
 DR InterPro; IPR003599; I9.
 DR InterPro; IPR007110; I9-like.
 DR InterPro; IPR003596; I9_v.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR NON_TER 196
 FT 196
 SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 76.5%; Score 523; DB 2; Length 196;
 Best Local Similarity 86.2%; Pred. No. 3.6e-43;

Matches 100; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVQCEKRVESGGGLVPGASLKISCAASGFTFSNYGMSWVRQTS 60
 Db 1 MNFGSLIFLVVLKGVQCEKRVESGGGLVPGASLKISCAASGFTFSNYGMSWVRQTP 60
 61 DKRLFWVASISGSDSTFYADNVKGRFTISRNAKNTLYLQMSLSKSEDTALYYCA 116
 Db 61 EKRLFWVASISGSGSYTYPPDVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCA 116

RESULT 5

HV54_MOUSE
 ID HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: This sequence belongs to the VHT183 subfamily.
 DR PIR; JTO505; HVMS84.
 DR HSSP; P01810; 2FBI.

DR InterPro; IPR007110; I9-like.
 DR InterPro; IPR003596; I9_v.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DN Immunoglobulin V region; Signal.
 FT SIGNAL 19
 FT CHAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 75.6%; Score 517; DB 1; Length 117;
 Best Local Similarity 85.5%; Pred. No. 7.9e-43;
 Matches 100; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVQCEKRVESGGGLVPGASLKISCAASGFTFSNYGMSWVRQTS 60
 Db 1 MNFGSLIFLVVLKGVQCEKRVESGGGLVPGASLKISCAASGFTFSNYGMSWVRQTP 60
 61 DKRLFWVASISGSDSTFYADNVKGRFTISRNAKNTLYLQMSLSKSEDTALYYCAR 117
 Db 61 EKRLFWVASISGSGSYTYPPDVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCAR 117

RESULT 6

HV55_MOUSE
 ID HV55_MOUSE STANDARD; PRT; 117 AA.
 AC P18526;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 345 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: This sequence belongs to the VHT183 subfamily.
 DR HSSP; P01783; IIGC.
 DR InterPro; IPR007110; I9-like.
 DR InterPro; IPR003596; I9_v.
 DR Pfam; PF00047; I9; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DN Immunoglobulin V region; Signal.
 FT SIGNAL 19
 FT CHAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 75.3%; Score 515; DB 1; Length 117;
 Best Local Similarity 84.6%; Pred. No. 1.2e-42;
 Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 MNFGLSLIFLVVLKGVQCEVKVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGLRLIFVLTKGVKCEVQVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRENAKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKRLWVASISGGSTYYPDVYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
HVS9_MOUSE
ID HVS9_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BA1B/CJ;
RC MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCLEANEUS: This sequence belongs to the VH7.83 subfamily.
DR HSSP; P18529; 118K.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT DOMAIN 20 117 Ig heavy chain V region 7-39.
FT DOMAIN 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULPID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;
Query Match 74.6%; Score 510; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 3.9e-42;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 1 MNFGLSLIFLVVLKGVQCEVKVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGLSLIFVLTKGVKCEVQVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRENAKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKRLWVASISGGSTYYPDVYKGRFTISRDNKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 8
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C2ECH II; TISSUE=Mammary tumor;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Strausberg R.L., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C2ECH II; TISSUE=Mammary tumor;
RC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010327; AAH10327.1; -.
DR PIR; S68213; S68213.
DR HSSP; P01783; 110C.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00406; CYTOCHROME_C; 4.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932A12 CRC64;
Query Match 74.6%; Score 510; DB 2; Length 473;
Best Local Similarity 71.5%; Pred. No. 1.8e-41;
Matches 98; Conservative 19; Mismatches 16; Indels 4; Gaps 1;
QY 1 MNFGLSLIFLVVLKGVQCEVKVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDSRLNIVFLVLTKGVQCEVQVYSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQAP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRENAKNTLYLQMSLSKSEDTALYYCAR-- 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKLEWVASISGGSTTYADTYKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARLEW 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 --DLFWNGGTTLVSS 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 LRRIDYWGQGTITLVSS 137
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 9
Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein (Fragment).
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

```

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=FVB/N; TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Struhsberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010798; AAH10798.1; -
 DR HSSP; P01789; IMCP.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR NON_TER 1
 FT SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 73.5%; Score 502.5; DB 2; Length 480;
 Best Local Similarity 72.6%; Pred. No. 9.8e-41;
 Matches 98; Conservative 17; Mismatches 17; Indels 3; Gaps 1;
 QY 2 NFGSLIFLVLYLVKGVQCEVYVSGGGLVKKPGASLKLSCAASGFTFSNYGMSVWROTSD 61
 DB 1 NFGSLIFLVLYLVKGVQCEVYVSGGGLVKKPGASLKLSCAASGFTFSNYGMSVWROTSD 60
 QY 62 KLELVVASISSGGSTFYADNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDL 121
 DB 61 KLELVVASISSGGSTFYADNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDL 120
 QY 122 N---WGQGTTLTVSS 133
 DB 121 YFDVWAGATTVTSS 135

RESULT 10
 Q6PDB8 PRELIMINARY; PRT; 485 AA.
 AC Q6PDB8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 OS Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Struhsberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058814; AAH58814.1; -
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003606; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 FT SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 72.3%; Score 494.5; DB 2; Length 485;
 Best Local Similarity 69.3%; Pred. No. 6e-40;
 Matches 97; Conservative 16; Mismatches 20; Indels 7; Gaps 1;
 QY 1 MNFGLSIFLVLYLVKGVQCEVYVSGGGLVKKPGASLKLSCAASGFTFSNYGMSVWROTSD 60
 DB 1 MDSRFLVFLVLYLVKGVQCEVYVSGGGLVKKPGASLKLSCAASGFTFSNYGMSVWROTSD 60
 QY 61 DRLLEWVASISSGGSTFYADNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDL 120
 DB 61 EKGLWVAVYISSSGSTFYADNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDL 120
 QY 121 FN-----WGQGTTLTVSS 133
 DB 121 SNYGGAMDYWGQGTSTVTVSS 140

RESULT 11
 HV53 MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region RF precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/cj;
 MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response." J. Exp. Med. 169:2007-2019 (1989).

CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR HSP: P18529; 118K.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG LIKE; 1.

KW Hybridoma; Immunoglobulin V region; Signal.

FT SIGNAL 1

FT CHAIN 20 117 Ig heavy chain V region RF.

FT DOMAIN 20 49 Framework-1.

FT DOMAIN 50 54 Complementarity-determining-1.

FT DOMAIN 55 68 Framework-2.

FT DOMAIN 69 85 Complementarity-determining-2.

FT DOMAIN 86 117 Framework-3.

FT DISULFID 41 115 By similarity.

FT NON TER 117 117

SO SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 72.1%; Score 493; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 1.8e-40;
Matches 98; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVLYLVKGVQCEVKYVESGGGLVPGASLKISCAASGFTPSNYGMSWRQTS 60
Db 1 MNGGLRIFLVLYLVKGLVQCEVKYVESGGGLVPGASLKISCAASGFTPSNYGMSWRQTS 60

QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRENKNTLYLQMSLSKSEDTALYYCAR 117
Db 61 EKRLWVAALNSNGSGSTYFPDVTYGRFTISRDNKNTLYLQMSLSKSEDTALYYCAR 117

RESULT 12

Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1;

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE IGHM protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Cannici P., Prange C.,
RA Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC020240; AAH02040.1; -

DR PIR: P36005; P36005.

DR PIR: G36005; G36005.

DR PIR: PH1642; PH1642.

DR PIR: PH1643; PH1643.

DR PIR: PH1645; PH1645.

DR PIR: PH1646; PH1646.

DR PIR: PL0098; PL0098.

DR PIR: PL0120; PL0120.

DR PIR: S15590; S15590.

DR PIR: S31116; S31116.

DR PIR: S31119; S31119.

DR PIR: S70442; S70442.

DR HSP: P01861; IADQ.

DR Pfam: PF07654; Cl-se; 4.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG LIKE; 5.

DR PROSITE: PS00290; IG MHC; UNKNOWN 3.

SO SEQUENCE 613 AA; 67295 MW; 60C7F5950671B315 CRC64;

Query Match 71.9%; Score 492; DB 2; Length 613;
Best Local Similarity 67.6%; Pred. No. 1.4e-39;
Matches 94; Conservative 23; Mismatches 16; Indels 6; Gaps 2;

QY 1 MNFGSLIFLVLYLVKGVQCEVKYVESGGGLVPGASLKISCAASGFTPSNYGMSWRQTS 60
Db 1 MNGGLRIFLVLYLVKGLVQCEVKYVESGGGLVPGASLKISCAASGFTPSNYGMSWRQTS 60

QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRENKNTLYLQMSLSKSEDTALYYCAR-- 118
Db 61 GKRLWVAIVISDGSNKYYADSVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCAKDS 120

QY 119 ---DLFN-WGQGTTLTVSS 133
Db 121 EGVETFDIWGGQTMVTVSS 139

RESULT 13

HV58 MOUSE STANDARD; PRT; 117 AA.

AC HV58 MOUSE;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig heavy chain V region 5-76 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/cJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response." J. Exp. Med. 169:2007-2019 (1989).

CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR: J70506; HWS57.

DR PDB: 1181; X-ray; B=20-117.

DR PDB: 118K; X-ray; B=20-117.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG LIKE; 1.

KW 3D-structure; Immunoglobulin V region; Signal.

FT SIGNAL 1 19 Ig heavy chain V region 5-76.

FT CHAIN 20 117

```
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78BFA0 CRC64;

Query Match 71.8%; Score 491; DB 1; Length 117;
Best Local Similarity 80.3%; Pred. No. 2.8e-40;
Matches 94; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVYLKGVQCEVKVVGSGGLVPRGASLKISCAASGFTFSNYGMSVTRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MNFVLSLIFLALTLKVGQCEVHLVBSGGGLVPRGSLKISCVSGTTFNKYAMSVWRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DKRLKLVASISGGSGSTFPADVNGKRFITSRNANNTLYLQMSLSKSEDTALYYCAR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKRLKLVATISSGGLVTPYDVKGRFTISRDNAGNTLYLQMSLSKSEDTALYYCAR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
O6GMV2 PRELIMINARY; PRT; 606 AA.
ID O6GMV2
AC O6GMV2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
   [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -
DR InterPro; IPR003599; IG_
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_1like.
DR InterPro; IPR003596; IG_1like.
DR Pfam; PF07654; CI-sect. 4.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IG1; 4.
```

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypoetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114B4C55 CRC64;

Query Match 71.3%; Score 488; DB 2; Length 606;
Best Local Similarity 62.7%; Pred. No. 3.3e-39;
Matches 96; Conservative 20; Mismatches 17; Indels 20; Gaps 2;

QY 1 MNFGSLIFLVYLKGVQCEVKVVGSGGLVPRGASLKISCAASGFTFSNYGMSVTRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEFGSLWFLVALIKGVQCEVQLVBSGGGLVPRGSLRLISCAASGFTFSNYGMSVTRQAP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DKRLKLVASISGGSGSTFPADVNGKRFITSRNANNTLYLQMSLSKSEDTALYYCAR 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GKGLKLVASISGGSGSTFPADVNGKRFITSRNANNTLYLQMSLSKSEDTALYYCAR 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 -----DLPN-----WGQGTTLTVSS 133
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GIAAGRVVYADYYVYGGMDVGGGTTVSS 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
O96BB9 PRELIMINARY; PRT; 597 AA.
ID O96BB9
AC O96BB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
   [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSP; F01861; IAD0.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_1like.
DR Pfam; PF07654; CI-sect. 4.
```

DR SMART; SM00406; IG^v: 1
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS02090; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCADAD8ECE263D9 CRC64;

Query Match	71.3%	Score	487.5	DB 2	Length	597			
Best Local Similarity	63.7%	Pred	No.3.7e-39						
Matches	93	Conservative	24	Mismatches	14	Indels	15	Gaps	2

```

0Y 1 NMFGLSLFLVAVILKGVCEVKEVKEGGGIVYRGASIKLSCASGGTFNSYGMWROTS 60
Db 1 MEFGLSWLFLVAILKGVCEVQVLLSGGGIVDPGSLRISCASGHSFSSYAMWVRQAP 60
0Y 61 DKRLFEWVASISSGSDSTFYADNVKRGFTTSRENAKQTIYLOMSSLSRDPALYYCARD -- 118
Db 61 GKGLFWVASAISSGSGSTYYADSVKGFFTTSRDSNRDITLYOMNSLRAEDTAVYYCAK DPR 120
0Y -----DLFNNGGQGTLLTVSS 133
Db 121 GYSASGNTRYREDY--MGQGTLLTVSS 144

```

Search completed: May 25, 2005, 15:56:04
Job time : 65.8298 secs